

178167

From: Whiteman, Brian
Sent: Tuesday, January 31, 2006 12:55 PM
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10/725,013

SEQ ID NO: 2

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Remsen, 2D14
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Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
(571) 272-0764

Searcher: _____
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Date Searcher Picked up: _____
Date completed: _____
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Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
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Other (Specify): _____

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OM protein - protein search, using sw model

Run on: February 4, 2006, 04:45:13 ; Search time 16 Seconds
(without alignments)
420.365 Million cell updates/sec

Title: US-10-725-013-2
Perfect score: 3203
Sequence: 1 MLGVLVIGALALAGLGPAP.....APSKVVLQHVTRTFRQL 574

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep:.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep:.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep:.*
4: /cgn2_6/ptodata/2/pubpaa/PCF_NEW_PUB pep:.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep:.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep:.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep:.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3176.5	99.2	631	US-10-995-561-546	Sequence 546, App
2	587.5	18.3	652	US-10-821-234-1016	Sequence 1016, App
3	426	13.3	1664	US-10-055-877-212	Sequence 212, App
4	414.5	12.9	1574	US-10-055-877-211	Sequence 211, App
5	411	12.8	1620	US-10-055-877-213	Sequence 213, App
6	386	12.1	1198	US-10-453-372-880	Sequence 880, App
7	386	12.1	1398	US-10-055-877-46	Sequence 872, App
8	386	12.1	1398	US-10-453-372-872	Sequence 46, App
9	386	12.1	1450	US-10-055-877-48	Sequence 48, App
10	386	12.1	1450	US-10-453-372-874	Sequence 874, App
11	386	12.1	1594	US-10-453-372-860	Sequence 860, App
12	384	12.0	2871	US-11-169-041-131	Sequence 131, App
13	384	12.0	3002	US-10-821-234-916	Sequence 916, App
14	379.5	11.8	1403	US-10-055-877-52	Sequence 52, App
15	379.5	11.8	1403	US-10-453-372-878	Sequence 878, App
16	379.5	11.8	1404	US-10-055-877-44	Sequence 44, App
17	379.5	11.8	1404	US-10-453-372-870	Sequence 870, App
18	379.5	11.8	1547	US-10-453-372-886	Sequence 886, App
19	379.5	11.8	1577	US-10-055-877-54	Sequence 54, App
20	379.5	11.8	1577	US-10-453-372-882	Sequence 882, App
21	379.5	11.8	1620	US-10-453-372-884	Sequence 884, App
22	379.5	11.8	1620	US-10-453-372-868	Sequence 868, App
23	379.5	11.8	1653	US-10-453-372-866	Sequence 866, App
24	373	11.6	1418	US-10-453-372-864	Sequence 864, App
25	358.5	11.2	956	US-11-113-424-39	Sequence 39, App

26	350	10.9	915	US-10-131-826A-294	Sequence 294, App
27	348.5	10.9	1902	US-10-453-372-1004	Sequence 1004, App
28	337.5	10.5	999	US-11-113-424-36	Sequence 36, App
29	335	10.5	993	US-11-137-465-36	Sequence 36, App
30	332.5	10.4	997	US-11-080-991-50	Sequence 50, App
31	332.5	10.4	4995	US-10-453-372-1002	Sequence 1002, App
32	330.5	10.3	897	US-11-137-465-35	Sequence 35, App
33	328	10.2	961	US-11-113-424-35	Sequence 35, App
34	325	10.1	1400	US-10-821-234-1045	Sequence 1045, App
35	323	10.1	965	US-11-113-424-2	Sequence 2, App
36	322	10.1	964	US-11-137-465-58	Sequence 58, App
37	322	10.1	965	US-11-147-047-51	Sequence 51, App
38	321	10.0	443	US-10-131-826A-318	Sequence 318, App
39	315	9.8	602	US-10-453-372-1064	Sequence 1064, App
40	313.5	9.8	997	US-11-113-424-37	Sequence 37, App
41	310.5	9.7	703	US-10-821-234-1412	Sequence 1412, App
42	296.5	9.3	387	US-11-137-465-57	Sequence 57, App
43	295	9.2	493	US-11-169-041-157	Sequence 157, App
44	295	9.2	497	US-10-821-234-1119	Sequence 1119, App
45	280.5	8.8	2471	US-11-050-346-68	Sequence 68, App

ALIGNMENTS

RESULT 1
US-10-995-561-546
; Sequence 546, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARIGLIU, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 546
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-995-561-546

Query Match	99.2%	Score 3176.5	DB 6	Length 631
Best Local Similarity	99.5%	Pred. No. 1.2e-215		
Matches 572	Conservative 0	Mismatches 2	Indels 1	Gaps 1
QY	1	MLGVLVIGALALAGLGPAPAEPOPGSGQCEHDCPALYPGPATFLNASQICDGLRGHLM	60	
DB	57	MLGVLVIGALALAGLGPAPAEPOPGSGQCEHDCPALYPGPATFLNASQICDGLRGHLM	116	
QY	61	TVRSVADYVSLIANGDGVGRRRLWIGLQIPGCGDPKRLGDLGPFQVWVGNNNTSYS	120	
DB	117	TVRSVADYVSLIANGDGVGRRRLWIGLQIPGCGDPKRLGDLGPFQVWVGNNNTSYS	176	
QY	121	RMARLDNGAPLCPGLCVAAAEATVPSEPIWEOOCVYKASFLCEHFPPATCRPLAV	180	
DB	177	RMARLDNGAPLCPGLCVAAAEATVPSEPIWEOOCVYKASFLCEHFPPATCRPLAV	236	
QY	181	EPGAAAASVITVGTTPPAAGADFOALPVSSAAVAPLGLQIMCTAPGAVOGHMAEAP	240	
DB	237	EPGAAAASVITVGTTPPAAGADFOALPVSSAAVAPLGLQIMCTAPGAVOGHMAEAP	296	
QY	241	GAMDCSYENGSCCHCAIIGAPRCQCPAGALQADGRSCTAS-TOSCNDCIHFVCVNP	299	
DB	297	GAMDCSYENGSCCHCAIIGAPRCQCPAGALQADGRSCTASATOSCNDCIHFVCVNP	356	
QY	300	DQPSYSVCMETGRIAADGRCDNDCTLESPPCQRCVNVNQGFECHPYVDLVG	359	
DB	357	DQPSYSVCMETGRIAADGRCDNDCTLESPPCQRCVNVNQGFECHPYVDLVG	416	

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Qy 360 ECVFVDFCFRANCEYOCQPLNQTSLVCVCAEGFAP1PHEBHRCOMFCNQACPADCDPN 419
| | | | |
Db 417 ECVFVDFCFRANCEYOCQPLNQTSLVCVCAEGFAP1PHEBHRCOMFCNQACPADCDPN 476
| | | | |
Qy 420 TOASCCEBEGYIILDDGFCTDIDECENGCFSSGVCHNLPFFETICGPDALARIHTGDC 479
| | | | |
Db 477 TOASCCEBEGYIILDDGFCTDIDECENGCFSSGVCHNLPFFETICGPDALARIHTGDC 536
| | | | |
Qy 480 DSGVDDGSDSGSPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALCHLR 539
| | | | |
Db 537 DSGVDDGSDSGSPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALCHLR 596
| | | | |
Qy 540 KKGGAARAKMEYKCAAPSEVVLQHVTRTERTPORL 574
| | | | |
Db 597 KKGGAARAKMEYKCAAPSEVVLQHVTRTERTPORL 631
| | | | |

RESULT 2
US-10-821-234-1016
; Sequence 1016, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andaman, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_version 1.0
; SEQ ID NO 1016
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1016

Query Match 18.3%; Score 587.5; DB 6; Length 652;
Best Local Similarity 31.5%; Pred. No. 2,7e-34;
Matches 179; Conservative 57; Mismatches 210; Indels 123; Gaps 31;

Qy 2 LGVILVGLALALA--GLGPPAPAEPPQGSQCYEHDCFLYPPPAFTPLNASTQICDGLRHL 59
| | | | |
Db 5 MCLLLLLLLLLLTOPGAGTGADTE---AVVCVGTACTYHSGKTLAAEAKHNNCHNNGSL 60
| | | | |
Qy 60 MIVRASSVAD----VLSLLNDGGVGR--RLMTGLQLPFG--CGDPKRLGFLRGFOWT 112
| | | | |
Db 61 ATVKSRKEKQHVQRYLAQLLRREALTAMSKFHWGLQREKCKLDPSL--PLKGFHWG 118
| | | | |
Qy 113 GNNNTSYSMARLDLNGAPLGLCVVA--VSAEATVPSE--PIWEBOC-----EVKA 163
| | | | |
Db 119 GEDBTPIYSWMKELNSC--ISKRCVSLLDLSQPLRLKMSBEGPSSGSPGNSIN 176
| | | | |
Qy 164 GFLCFHPATCRPLAV--EPGAAAAVSTTGTTPPAKGAQFQALPVSSAAVAPLGLQL 222
| | | | |
Db 177 GFVCKFSFGMCRPLALGSPG-----QVTTYTPFTTSSLEAVFPAALVA----- 224
| | | | |
Qy 223 MC-TAPPGAVQHW---AREAPGAM-----CSVENGGCHAC--NALPGAR 263
| | | | |
Db 225 -CGEGDKBTQSHYFLCKEKAPDVFWMGSSGPLCVSPKYGCFNNNGCHQDFEGGDSF 283
| | | | |
Qy 264 PQCCPAGALADAGRECTASTGSCNLCB--HFCVNPPOPGSSYSCMCTGYRLADQHR 321
| | | | |
Db 284 LGGCRGFRLLDLVTCASRNPCSSSPCGGATCVLGP--HGKNTCRCPQGQQLDSSQLD 342
| | | | |
Qy 322 CEVDVDCILBPPCPPCPCPCVNTGSGFCHCYPNYDLVAGSCVEVDFCFRANCEYOCQPLN 381
| | | | |
Db 343 CVDVDECC--QDSFCAOBCVNTPGSFCECMVG-----EGGCP-----GGGACQDND 387
| | | | |
Qy 382 QTSYLCVCAEGFAP1PHEBHRCOMFCNQACPADCDPNTOAS--CECPBEGYIIL--DDGFI 437
| | | | |
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Db 388 E-----CALGRP-----CAQGC--TNTDGSFRCCEBEGYVLAGSDGTQ 424
| | | | |
Qy 438 CTDIDEC--ENGFCSGVCHNLPFFETICGPDALARIHTGDCSGKV-----DG 486
| | | | |
Db 425 CQDVDECVGSGFLCDBSLCFTNTGSGFHCGLFCMVLAAPN--GVSCTWGPPVSLGPPSGPDE 483
| | | | |
Qy 487 GDSGSGE-----PPSPPTGSLTPPA 508
| | | | |
Db 484 EDKKEKESVTPPRAATASPTRGSGTTPKA 512
| | | | |

RESULT 3
US-10-055-877-212
; Sequence 212, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Vellizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Rameesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zethusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eiden, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Sureeh
; APPLICANT: Li, Li
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Renée
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
```

SEQ ID NO 212
 LENGTH: 1664
 TYPE: PRT
 ORGANISM: Caenorhabditis elegans
 US-10-055-877-212

Query Match 13.3%; Score 426; DB 6; Length 1664;
 Best Local Similarity 27.7%; Pred. No. 1.4e-22;
 Matches 138; Conservative 49; Mismatches 200; Indels 112; Gaps 23;

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QY YSRMARLDNGAPLGGPLCVAVSAAB-----ATVPSPIEBOQCE--VAADGLTGF 169
DB 56 YLRFRPSRRGSKCCLRVQANCSADLCHNGTCSPSHNDNEQVCECPVGTAKCY 115
QY 170 HPPATCRPLAVPAGAAAVSITTYTPFARGADQALPVGSSAAVAPLGLQIMCTAPPG 229
DB 116 D-ANNC--MANNGGHEHCYN--TIGTY-----CRCPWG 145
QY 230 AVQGHMAREAPGANDCSVENGGCEHAQNAIPGAPPCQCPAGAAQADGRSC----- 280
DB 146 FELSGDGNVTSIDIDCAVANGGCSDRCVNSPGFRCDCPSDLYLHADGRTCGSGFHEML 205
QY 281 -----TASTQSGNDLCEHFCVNPDPQSGYSCKETGRLADQHRCEVDVDCILPSPBC 335
DB 206 ILIKKVTSCSTDNGGCEHEC--ENDNGEFYRCRCVGFGLSENKSCQPVDPFDPNKGQC 264
QY 336 FORCVNTQGFECFCYPNYDL--VDGEVCEVPDPCFRAN--CEYQCCPLNQTSYLCVCAEGF 393
DB 265 QHCHNNHGRACQCYPGFHLSDYDRSCVDIDCKANNCEHFCENVKGTYRCKRREY 323
QY 394 APIPEHRCQMF-----CNQTPACPAD--DPNTQASCECPGYLL--DGFICTDIDSC- 444
DB 324 -QLGRDRTCEMLGGCQVANGGCGHDCDQDGDGHVCKCRNGYLLANDQKLDHINBEH 382
QY 445 ENGECFCVCHNLPTFEFCICPDSALAHITF-----DCSGKVDG-----DSGSEP 494
DB 383 ENNGDCSQICVNLGASVBCQCKPGLMKDRKTCDISCSN--NGGEOQICSNQEGGY 440
QY 495 PPSPTGSTLTPPANG-----LVHSGLLIGISTASLCVVALALCHLKKQGAAR- 546
DB 441 MCSCEPPELSEBDGSHCDNMECLINNG-----GCAQLC-----KRRKGRRC 483
QY 547 -----AKMEYKCAAPS 557
DB 484 QCFAGYILAHDEKSCVAAS 502

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RESULT 4
 US-10-055-877-211
 ; Sequence 211, Application US/10055877
 ; Publication No. US20050288241A1

GENERAL INFORMATION:

APPLICANT: Decristofaro, Marc
 APPLICANT: Padigaru, Muralidhara
 APPLICANT: Miller, Charles
 APPLICANT: Tcherny, Velizar
 APPLICANT: Zhong, Mei
 APPLICANT: Anderson, David
 APPLICANT: Ballinger, Robert
 APPLICANT: Gerlach, Valerie
 APPLICANT: Spytek, Kimberly
 APPLICANT: Ratelli, Luca
 APPLICANT: Kekuda, Ramesh
 APPLICANT: Guo, Xiaojia
 APPLICANT: Zetunuen, Bryan
 APPLICANT: Andrew, David
 APPLICANT: Mezes, Peter
 APPLICANT: Paturajan, Meera
 APPLICANT: Burgess, Catherine
 APPLICANT: Eisen, Andrew
 APPLICANT: Wolenc, Adam
 APPLICANT: Baumgartner, Jason
 APPLICANT: Shimkets, Richard

APPLICANT: Gusev, Vladimir
 APPLICANT: Vernet, Corine
 APPLICANT: Taupier Jr., Raymond
 APPLICANT: Pena, Carol
 APPLICANT: Shenoy, Suresh
 APPLICANT: Li, Li
 APPLICANT: Casman, Stacie
 APPLICANT: Boldog, Ferenc
 TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
 FILE REFERENCE: 21402-251
 CURRENT APPLICATION NUMBER: US/10/055,877

CURRENT FILING DATE: 2002-01-22
 PRIOR APPLICATION NUMBER: 60/262,892
 PRIOR FILING DATE: 2001-01-19
 PRIOR APPLICATION NUMBER: 60/263,598
 PRIOR FILING DATE: 2001-01-23
 PRIOR APPLICATION NUMBER: 60/263,799
 PRIOR FILING DATE: 2001-01-24
 PRIOR APPLICATION NUMBER: 60/264,117
 PRIOR FILING DATE: 2001-01-25
 PRIOR APPLICATION NUMBER: 60/264,139
 PRIOR FILING DATE: 2001-01-25
 PRIOR APPLICATION NUMBER: 60/264,478
 PRIOR FILING DATE: 2001-01-26
 PRIOR APPLICATION NUMBER: 60/263,351
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: 60/272,870
 PRIOR FILING DATE: 2001-03-02
 PRIOR APPLICATION NUMBER: 60/275,990
 PRIOR FILING DATE: 2001-03-14
 PRIOR APPLICATION NUMBER: 60/275,927
 PRIOR FILING DATE: 2001-03-14
 Remaining Prior Application data removed - See file wrapper or PALM.
 NUMBER OF SEQ ID NOS: 512
 SOFTWARE: Patent Ver. 2.1
 SEQ ID NO 211
 LENGTH: 1574
 TYPE: PRT
 ORGANISM: Rattus norvegicus
 US-10-055-877-211

Query Match 12.9%; Score 414.5; DB 6; Length 1574;
 Best Local Similarity 34.2%; Pred. No. 8.4e-22;
 Matches 104; Conservative 28; Mismatches 101; Indels 71; Gaps 17;

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QY 224 CTAPPG-AVQGHMAREAGANDCSVENGGCEHACHAATGAPPCQCPAGAAQADGRSCTA 282
DB 147 CRCPGYQLQGD--GTCODVDCEAHNGGCGHRCVNTGYSYLCECKPGLHTDERTCIA 205
QY 283 STQSC--NDCEHFCVP-----NPDQPGYSYCM----- 308
DB 206 -ISSCTLANGGCQHCQVOLLTYTHRCQCRPRQYQLQEDGRRCVRRSPCAEGNGGCHNIOE 264
QY 309 -----CETGYRLADQHRCEVDVDCILPSPCPQCVNTQSGFECYPNYDL--VDG 359
DB 265 LRGLAHGCHHGYQLAADRKTCEDVDSCALGLAQAHGCLNTQGSFKVCVAGYELGADG 324
QY 360 -EC---VEVPDPCFRAN--CEYQCCPLNQTSYLCVCAEGFAPLTPHEHRCQMF----- 407
DB 325 RQCYRIEWEIVNSCEAGNGGCSHGCSH--TSGPLCTCPRGY-----ELDEQKTCIDID 378
QY 408 --NOTACPADDDPTQA--SCECPGYLLD--DGFICTDIDCENG--GFCSGVCHNLPGTF 461
DB 379 CANSPPCCQAC--ANTPGSYSCFAGRYLNTDGGCGCEVDVCAQSHGGCHHCSNLAGSF 437
QY 462 ECIC 465
DB 438 QCFC 441

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RESULT 5
 US-10-055-877-213
 ; Sequence 213, Application US/10055877

```
/ Publication No. US20050286241A1
/ GENERAL INFORMATION:
/ APPLICANT: Decristofaro, Marc
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Miller, Charles
/ APPLICANT: Tchiernev, Velizar
/ APPLICANT: Zhong, Mei
/ APPLICANT: Anderson, David
/ APPLICANT: Ballinger, Robert
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Kexuda, Ramesh
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Zernusen, Bryan
/ APPLICANT: Andrew, David
/ APPLICANT: Mezes, Peter
/ APPLICANT: Paturajan, Meera
/ APPLICANT: Burgess, Catherine
/ APPLICANT: Eiseen, Andrew
/ APPLICANT: Wolenc, Adam
/ APPLICANT: Baumgartner, Jason
/ APPLICANT: Shinkets, Richard
/ APPLICANT: Gusev, Vladimir
/ APPLICANT: Vernet, Corine
/ APPLICANT: Taupier Jr., Raymond
/ APPLICANT: Pena, Carol
/ APPLICANT: Shenoy, Sureeh
/ APPLICANT: Li, Li
/ APPLICANT: Caeman, Stacie
/ APPLICANT: Boldog, Ference
/ TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
/ FILE REFERENCE: 21402-251
/ CURRENT APPLICATION NUMBER: US/10/055,877
/ CURRENT FILING DATE: 2002-01-22
/ PRIOR APPLICATION NUMBER: 60/262,892
/ PRIOR FILING DATE: 2001-01-19
/ PRIOR APPLICATION NUMBER: 60/263,598
/ PRIOR FILING DATE: 2001-01-23
/ PRIOR APPLICATION NUMBER: 60/263,799
/ PRIOR FILING DATE: 2001-01-24
/ PRIOR APPLICATION NUMBER: 60/264,117
/ PRIOR FILING DATE: 2001-01-25
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/ PRIOR APPLICATION NUMBER: 60/264,478
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/ PRIOR APPLICATION NUMBER: 60/263,351
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/272,870
/ PRIOR FILING DATE: 2001-03-02
/ PRIOR APPLICATION NUMBER: 60/275,990
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/275,927
/ PRIOR FILING DATE: 2001-03-14
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 512
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 213
/ LENGTH: 1620
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
/ US-10-055-877-213

Query Match      12.8%; Score 411; DB 6; Length 1620;
Best Local Similarity 25.9%; Pred. No. 1,5e-21;
Matches 142; Conservative 47; Mismatches 197; Indels 162; Gaps 25;

Cy      119 YSRMARLNLGNAPLGGPVCVANSAAE-----ATVPSRPPIREQQCE--VVAADGFLCBF 169
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      56 YLRFARFRRRGGKCCCLLRQANCSADLCCHNGGTCPSEHNDNEQVCECPVFTAKKCY 115
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Cy      170 HFPATCRPLAVPGAAAAAASITVGTFFAARGADFOALPVGSSAAVAPLGLQIMCTAPPG 229
```

```
Db      116 D-ANEC--MANNGCCHECVN-TIGITY-----CRCWPG 145
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Cy      230 AVQGHMAREAPGAWDCSVENGCEHACNAIPGARPCQCPAGAAIQADGRSCTASTGSC-- 287
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      146 FELSGDNTGSDIDIECAVNSGGSDRCVNSPGRRCPCPSFDLYLHADGRTCGKVT-SCST 204
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Cy      288 -NDLCHEFCVPNPQPSYSQCMETGYRLAADQRCEVDVDCILFSPPCPRQCVNTOGGF 346
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      205 DNGGCEHEC-ENDSNGEFTYRCRCRVGFKLSBNKRSQPVDPCCFDNKGCCQHHCTNNHGRA 263
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Cy      347 ECHCYPNYDL-VQGECEVPEVDPCEFRAN-CEYQCOPLNQTSTYLCVCAEGFAPIPHEPRQC 404
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      264 QCCCTPGFHLSYDRSCVDIDIECAKNNGCEHFCENVAGT-YRCRCREGY-QLGNDARTCE 321
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Cy      405 MF-----CNOTACPADC--DPTQASCECEGYTL----- 432
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      322 EMLGGCQVNGGCGCHDCYDQPDGSHVCKRNGYILANDQKLCNDNISVYIHARARLWDS 381
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Cy      433 -----DDGF-----ICTYIDEC-ENGFCSGVCH 455
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      382 YEIVTCVPTDITLCHKLCMLDSGHVOCFCDDGYELIDSKFCODINCHENNDCSQICV 441
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Cy      456 NLPGTFRCIGSPDALARHIGT-----DCDSGKYDGG-----DSGSGEPSPPTPGSTLT 505
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      442 NLAGSVBQCKPGRFLMKDRKTCIDISCSN--NGGCBQICSNQBGYMCSCPEFELS 499
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Cy      506 PPAVG-----LVHSGLLIGISTASLCLVVALALALCHLRKKQGAAR-----AKM 549
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      500 EDGHSCHDMNCECLINN-----GCAQLC-----KNRKGSRRCQCFAGYILAH 542
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Cy      550 EYKCAADS 557
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      543 EKSCVAAS 550
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```

```
RESULT 6
US-10-453-372-880
/ Sequence 880, Application US/10453372
/ Publication No. US20060003323A1
/ GENERAL INFORMATION:
/ APPLICANT: Alsebrook, et al.
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
/ FILE REFERENCE: 21402-589 A
/ CURRENT APPLICATION NUMBER: US/10/453,372
/ CURRENT FILING DATE: 2003-06-03
/ PRIOR APPLICATION NUMBER: 09/789390
/ PRIOR FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: 60/185967
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: 09/823187
/ PRIOR FILING DATE: 2001-03-29
/ PRIOR APPLICATION NUMBER: 60/195792
/ PRIOR FILING DATE: 2000-03-10
/ PRIOR APPLICATION NUMBER: 09/839446
/ PRIOR FILING DATE: 2001-03-19
/ PRIOR APPLICATION NUMBER: 60/199476
/ PRIOR FILING DATE: 2000-03-25
/ PRIOR APPLICATION NUMBER: 09/863776
/ PRIOR FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: 60/208263
/ PRIOR FILING DATE: 2000-05-31
/ PRIOR APPLICATION NUMBER: 09/939398
/ PRIOR FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: 60/227800
/ PRIOR FILING DATE: 2000-08-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1609
/ SOFTWARE: Cursaseqlist version 0.1
/ SEQ ID NO 880
/ LENGTH: 1198
/ TYPE: PRT
/ ORGANISM: Homo sapiens
```


;; PRIOR FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: 60/227800
;; PRIOR FILING DATE: 2000-08-25
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1609
;; SOFTWARE: curseqdist version 0.1
;; SEQ ID NO: 872
;; LENGTH: 1398
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-453-372-872

Query Match 12.1%; Score 386; DB 6; Length 1398;

Best Local Similarity 33.8%; Pred. No. 7.4e-20;
Matches 101; Conservative 27; Mismatches 107; Indels 64; Gaps 16;

QY 224 CTAPRGAVQGHMAEAPAMPQSVNNGGCEHACNAIPGAPQCGAGAAADAGSSCTAS 283
DB 143 CHCEPG-FQG--PRCQYDVDCRTHNGGQHRCVNTPSYCECKPGFRLHTDSRTCLA- 198
QY 284 TQSC---NDLCEHFCV-----PNPDQPS----- 304
DB 199 INSCALNGSGQHHCYQTLTIRHRCQCRPGFQLOEDGHNCRSPCANRNSCMHRCQV 258
QY 305 ---YSCWCTGYRLAADGHRCEVDVDCILBSPPCQRCVNTQSGFECCHYNYDL-VDG- 359
DB 259 RGLARCECHVGQYLAADGKACEDVDECAAGLAQCANHGLNTQSGFKVCVCHAGYELGADGR 318
QY 360 EC---VPRVPCRRAN--CEYQCPPLNQTSY--LCVCAEGPAPRPH--RCOMFCNQ 409
DB 319 QCYRIEMETVNSCEANNNGGCSHG---SHTSAGPLCTCPRGYELDTDRTICRRLCRQ 375
QY 410 TACPADCDPNTQA-SCECPREGYILD-DGFICTDIDECENG-GFCSGVCHNLPGTFECTIC 465
DB 376 PVLQGVCTNNBGGVCGCYAGYRLSADCGCGEDVDECASSRGCGEHHCTNLAGSFQCGC 434

RESULT 9

US-10-055-877-48

;; Sequence 48, Application US/10055877
;; Publication No. US20050288241A1
;; GENERAL INFORMATION:

;; APPLICANT: Decristofaro, Marc
;; APPLICANT: Padigaru, Muralidhara
;; APPLICANT: Miller, Charles
;; APPLICANT: Tcherny, Velizar
;; APPLICANT: Zhong, Mei
;; APPLICANT: Anderson, David
;; APPLICANT: Ballinger, Robert
;; APPLICANT: Gerlach, Valerie
;; APPLICANT: Spytek, Kimberly
;; APPLICANT: Ratelli, Luca
;; APPLICANT: Kekuda, Ramesh
;; APPLICANT: Guo, Xiaojia
;; APPLICANT: Zernusen, Bryan
;; APPLICANT: Andrew, David
;; APPLICANT: Mezes, Peter
;; APPLICANT: Patturajan, Weera
;; APPLICANT: Burgess, Catherine
;; APPLICANT: Elien, Andrew
;; APPLICANT: Wolenc, Adam
;; APPLICANT: Baumgartner, Jason
;; APPLICANT: Shinkels, Richard
;; APPLICANT: Gusev, Vladimir
;; APPLICANT: Vernet, Corine
;; APPLICANT: Taupier Jr., Raymond
;; APPLICANT: Pena, Carol
;; APPLICANT: Shenoy, Suresh
;; APPLICANT: Li, Li
;; APPLICANT: Caeman, Stacie
;; APPLICANT: Boldog, Ferenc
;; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
;; FILE REFERENCE: 21402-251

;; CURRENT APPLICATION NUMBER: US/10/055,877
;; CURRENT FILING DATE: 2002-01-22
;; PRIOR APPLICATION NUMBER: 60/262,892
;; PRIOR FILING DATE: 2001-01-19
;; PRIOR APPLICATION NUMBER: 60/263,598
;; PRIOR FILING DATE: 2001-01-23
;; PRIOR APPLICATION NUMBER: 60/263,799
;; PRIOR FILING DATE: 2001-01-24
;; PRIOR APPLICATION NUMBER: 60/264,117
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: 60/264,139
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: 60/264,478
;; PRIOR FILING DATE: 2001-01-26
;; PRIOR APPLICATION NUMBER: 60/263,351
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: 60/272,870
;; PRIOR FILING DATE: 2001-03-02
;; PRIOR APPLICATION NUMBER: 60/275,990
;; PRIOR FILING DATE: 2001-03-14
;; PRIOR APPLICATION NUMBER: 60/275,927
;; PRIOR FILING DATE: 2001-03-14
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 512
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 48
;; LENGTH: 1450
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-055-877-48

Query Match 12.1%; Score 386; DB 6; Length 1450;

Best Local Similarity 33.8%; Pred. No. 7.7e-20;
Matches 101; Conservative 27; Mismatches 107; Indels 64; Gaps 16;

QY 224 CTAPRGAVQGHMAEAPAMPQSVNNGGCEHACNAIPGAPQCGAGAAADAGSSCTAS 283
DB 143 CHCEPG-FQG--PRCQYDVDCRTHNGGQHRCVNTPSYCECKPGFRLHTDSRTCLA- 198
QY 284 TQSC---NDLCEHFCV-----PNPDQPS----- 304
DB 199 INSCALNGSGQHHCYQTLTIRHRCQCRPGFQLOEDGHNCRSPCANRNSCMHRCQV 258
QY 305 ---YSCWCTGYRLAADGHRCEVDVDCILBSPPCQRCVNTQSGFECCHYNYDL-VDG- 359
DB 259 RGLARCECHVGQYLAADGKACEDVDECAAGLAQCANHGLNTQSGFKVCVCHAGYELGADGR 318
QY 360 EC---VPRVPCRRAN--CEYQCPPLNQTSY--LCVCAEGPAPRPH--RCOMFCNQ 409
DB 319 QCYRIEMETVNSCEANNNGGCSHG---SHTSAGPLCTCPRGYELDTDRTICRRLCRQ 375
QY 410 TACPADCDPNTQA-SCECPREGYILD-DGFICTDIDECENG-GFCSGVCHNLPGTFECTIC 465
DB 376 PVLQGVCTNNBGGVCGCYAGYRLSADCGCGEDVDECASSRGCGEHHCTNLAGSFQCGC 434

RESULT 10

US-10-453-372-874

;; Sequence 874, Application US/10453372
;; Publication No. US20060003323A1
;; GENERAL INFORMATION:

;; APPLICANT: Alsobrook, et al.
;; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;; FILE REFERENCE: 21402-589 A
;; CURRENT APPLICATION NUMBER: US/10/453,372
;; CURRENT FILING DATE: 2003-06-03
;; PRIOR APPLICATION NUMBER: 09/789390
;; PRIOR FILING DATE: 2001-02-23
;; PRIOR APPLICATION NUMBER: 60/185967
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: 09/823187
;; PRIOR FILING DATE: 2001-03-29
;; PRIOR APPLICATION NUMBER: 60/195792


```
;; PRIOR FILING DATE: 2000-03-10
;; PRIOR APPLICATION NUMBER: 09/839446
;; PRIOR FILING DATE: 2001-03-19
;; PRIOR APPLICATION NUMBER: 60/199476
;; PRIOR FILING DATE: 2000-03-25
;; PRIOR APPLICATION NUMBER: 09/863776
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: 60/208263
;; PRIOR FILING DATE: 2000-05-31
;; PRIOR APPLICATION NUMBER: 09/939398
;; PRIOR FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: 60/227800
;; PRIOR FILING DATE: 2000-08-25
;; Remaining Prior Application data removed - See file Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1609
;; SOFTWARE: CursSeqList version 0.1
;; SEQ ID NO 874
;; LENGTH: 1450
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-453-372-874
```

```
Query Match      12.1%; Score 386; DB 6; Length 1450;
Best Local Similarity 33.8%; Pred. No. 7.7e-20;
Matches 101; Conservative 27; Mismatches 107; Indels 64; Gaps 16;
```

```
QY 224 CTAPPGAVQGHWAAREAPGAMDCSVENGCEHACNAIPGARPCQCPAGALQADGRSCTAS 283
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 143 CHCPFG-FQG--PRCQYDVDECRTHNGGCGQHRCVNTPGSYLCECKRGPRLHTDSRTCLA- 198
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 284 TQSC---NDLCEHFCV-----PNDQPGS----- 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 199 INSCALGNGGCGQHCVQLTTRHRCQCRPGFQLOEDGRHCVRRSPCANRNGSCMRQCV 258
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 305 ---VSCMCEYGRILADQHRCEVDVDCILBSPFCQRCVNTQSGFECICYPYDL-VDG- 359
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 259 RGLARCEHVGQQLADQKACEDVDCAAGLAQCHGCLNTQSGFKVCYCHAGYELGADGR 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 360 EC---VEVPDPCFRAN--CEYQCPPLNTQSY--LCVCAEGFAPLPHEPH--RCOMFCNQ 409
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 319 QCYRIEMEIIVNSCEANNNGCSHG---SHTSAGPLCTCPRGVELTDDRTICRRLCRQ 375
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 410 TACPADCPNTQA--SCEPREGIYLD-DGFICTDIDECENG--GFGSGVCHNLPTECTIC 465
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 376 PVLQGVCTNNPGYEGCGYAGYRLSADGCGCEDVDECCASSRGGCEHCHCTNLNLAGSFQSC 434
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 11
US-10-453-372-860
;; Sequence 860, Application US/10453372
;; Publication No. US2006000323A1
;; GENERAL INFORMATION:
;; APPLICANT: Alisobrook, et al.
;; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;; FILE REFERENCE: 21402-589 A
;; CURRENT FILING DATE: US/10/453,372
;; PRIOR APPLICATION NUMBER: 09/789390
;; PRIOR FILING DATE: 2001-02-23
;; PRIOR APPLICATION NUMBER: 60/185967
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: 09/823187
;; PRIOR FILING DATE: 2001-03-29
;; PRIOR APPLICATION NUMBER: 60/195792
;; PRIOR FILING DATE: 2000-03-10
;; PRIOR APPLICATION NUMBER: 09/839446
;; PRIOR FILING DATE: 2001-03-19
;; PRIOR APPLICATION NUMBER: 60/199476
;; PRIOR FILING DATE: 2000-03-25
;; PRIOR APPLICATION NUMBER: 09/863776
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: 60/208263
;; PRIOR FILING DATE: 2000-05-31
```

```
;; PRIOR APPLICATION NUMBER: 09/939398
;; PRIOR FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: 60/227800
;; PRIOR FILING DATE: 2000-08-25
;; Remaining Prior Application data removed - See file Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1609
;; SOFTWARE: CursSeqList version 0.1
;; SEQ ID NO 860
;; LENGTH: 1594
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-453-372-860
```

```
Query Match      12.1%; Score 386; DB 6; Length 1594;
Best Local Similarity 33.8%; Pred. No. 8.5e-20;
Matches 101; Conservative 27; Mismatches 107; Indels 64; Gaps 16;
```

```
QY 224 CTAPPGAVQGHWAAREAPGAMDCSVENGCEHACNAIPGARPCQCPAGALQADGRSCTAS 283
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 147 CHCPFG-FQG--PRCQYDVDECRTHNGGCGQHRCVNTPGSYLCECKRGPRLHTDSRTCLA- 202
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 284 TQSC---NDLCEHFCV-----PNDQPGS----- 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 203 INSCALGNGGCGQHCVQLTTRHRCQCRPGFQLOEDGRHCVRRSPCANRNGSCMRQCV 262
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 305 ---VSCMCEYGRILADQHRCEVDVDCILBSPFCQRCVNTQSGFECICYPYDL-VDG- 359
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 263 RGLARCEHVGQQLADQKACEDVDCAAGLAQCHGCLNTQSGFKVCYCHAGYELGADGR 322
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 360 EC---VEVPDPCFRAN--CEYQCPPLNTQSY--LCVCAEGFAPLPHEPH--RCOMFCNQ 409
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 323 QCYRIEMEIIVNSCEANNNGCSHG---SHTSAGPLCTCPRGVELTDDRTICRRLCRQ 379
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 410 TACPADCPNTQA--SCEPREGIYLD-DGFICTDIDECENG--GFGSGVCHNLPTECTIC 465
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 380 PVLQGVCTNNPGYEGCGYAGYRLSADGCGCEDVDECCASSRGGCEHCHCTNLNLAGSFQSC 438
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 12
US-11-169-041-131
;; Sequence 131, Application US/11169041
;; Publication No. US20060019284A1
;; GENERAL INFORMATION:
;; APPLICANT: Bristol-Myers Squibb Company
;; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
;; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
;; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
;; TITLE OF INVENTION: CELLS
;; FILE REFERENCE: 10001 NP
;; CURRENT APPLICATION NUMBER: US/11/169,041
;; CURRENT FILING DATE: 2005-06-28
;; PRIOR APPLICATION NUMBER: 60/584,405
;; PRIOR FILING DATE: 2004-06-30
;; NUMBER OF SEQ ID NOS: 527
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 131
;; LENGTH: 2871
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-169-041-131
```

```
Query Match      12.0%; Score 384; DB 7; Length 2871;
Best Local Similarity 29.0%; Pred. No. 2.1e-19;
Matches 130; Conservative 28; Mismatches 124; Indels 166; Gaps 25;
```

```
QY 244 DCSVENGGCEHACNAIPGARPCQCPAGALQADGRSCTASTQSCNDLCEHFCVNP----- 299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1200 ECSINNGCEFTCNSEGSYSCSCOPGFALMPDQRCST-----DIDE--CEDNPNICD 1250
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 300 -----DQGSYSQMCFCYGRILADQHRCEVDVDCILBSPFC--PQRCVNTQSGFECICYPN 353
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1251 GGQCTNIPGEYRCLCYGFMASBDMKTCVDVNECDLMPNICTLSTGTCENTKGSFTCHCDMG 1310
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
Qy 354 YDLVDGE--CYPEVDPC--FRANCEYOCQPLNQT-SYLCVCAEGFA-----PIPH 398
Db 1311 YSGKGTGCTD-INCEIGAHNCGKHAVCTNTAGSFKCSGPMIGDIGICTDLDECSN 1369
Qy 399 EPHRCQMFQNOATACPADCDPTQAS--CECEPGYILDDGFTCTDIDEC-EN-----446
Db 1370 GTHWCSQH-----ADC-KNTMGSYRCLCKEGY-TGSGFTCTDIDECSEMLNLCGNQC 1420
Qy 447 ---GGF-----CS-----GVCNLPGETPECICGPPSALAR 473
Db 1421 LNAFGTRCECDMGFVPSADKACEDIECSLPNLCVGTCHNLPGLRCRCEIGYELDR 1480
Qy 474 HIG-----TDCSGKVDGDSGSGEPPEPFGS-----TLTPAVGLV- 512
Db 1481 SGGNCTDVNECLDPTTCSGNCVN-----TPGSYICDCPPDFELNPTFRVGCVD 1528
Qy 513 -HSG-----LLIGISIASLCLVALLALCHLRKQGA-----A 545
Db 1529 TRSGNCYLDIRPRGDNQDTACSNELGVGVSRASC-----CSLCKAWGTPEMCPA 1579
Qy 546 RAKMEYKCAAPSK-----VYLQHV 565
Db 1580 VNTSEYKILCPGSGFRPNPTVILEDI 1607
```

RESULT 13

```
US-10-821-234-916
; Sequence 916, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Steache-Crain, Birgit
; APPLICANT: Andaman, Suean
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_genes Version 1.0
; SEQ ID NO 916
; LENGTH: 3002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-916
```

```
Query Match 12.0%; Score 384; DB 6; Length 3002;
Best Local Similarity 29.0%; Pred. No. 2,2e-19;
Matches 130; Conservative 28; Mismatches 124; Indels 166; Gaps 25;
```

```
Qy 244 DCSVENGCEHACNAIPGARPCQCPAGALQADGSCSTASTOSCNLDLCHFCVPPNP--- 299
Db 1331 ECSINWGGCEFTCTNSGSEYECSCOPGFALMPDORSCT-----DIDE--CEDPNICD 1381
Qy 300 -----DQGSYSCEMETGRLAADHRCSDVDDCLLEBPC-PQRCVMTQGGFECHCYN 353
Db 1382 GQGCNTNIGEXRCLCTYDGMASEDMKTCVNECDLNPNICLSGTCTENKGSFICHDMG 1441
Qy 354 YDLVDGE--CYPEVDPC--FRANCEYOCQPLNQT-SYLCVCAEGFA-----PIPH 398
Db 1442 YSGKGTGCTD-INCEIGAHNCGKHAVCTNTAGSFKCSGPMIGDIGICTDLDECSN 1500
Qy 399 EPHRCQMFQNOATACPADCDPTQAS--CECEPGYILDDGFTCTDIDEC-EN-----446
Db 1501 GTHWCSQH-----ADC-KNTMGSYRCLCKEGY-TGSGFTCTDIDECSEMLNLCGNQC 1551
Qy 447 ---GGF-----CS-----GVCNLPGETPECICGPPSALAR 473
Db 1552 LNAFGTRCECDMGFVPSADKACEDIECSLPNLCVGTCHNLPGLRCRCEIGYELDR 1611
Qy 474 HIG-----TDCSGKVDGDSGSGEPPEPFGS-----TLTPAVGLV- 512
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Db 1612 SGGNCTDVNECLDPTTCSGNCVN-----TPGSYICDCPPDFELNPTFRVGCVD 1659
Qy 513 -HSG-----LLIGISIASLCLVALLALCHLRKQGA-----A 545
Db 1660 TRSGNCYLDIRPRGDNQDTACSNELGVGVSRASC-----CSLCKAWGTPEMCPA 1710
Qy 546 RAKMEYKCAAPSK-----VYLQHV 565
Db 1711 VNTSEYKILCPGSGFRPNPTVILEDI 1738
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RESULT 14

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US-10-055-877-52
; Sequence 52, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigaru, Murailidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Rattel, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patburajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkels, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Scacie
; APPLICANT: Boldog, Ferenc
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 52
; LENGTH: 1403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-055-877-52

Query Match 11.8%; Score 379.5; DB 6; Length 1403;
Best Local Similarity 32.3%; Pred. No. 2.1e-19;
Matches 98; Conservative 31; Mismatches 105; Indels 69; Gaps 16;

QY 224 CTAPGAVQ---GHWAEAPGAMDCSVNGGCEHACNAIPGARPCQCPAGAAALQADGRS 279
DB 146 CRWPPSHQLOGDGETCODVD---ECRTHNGGCGHRCVNTPGSYLCECKPGFRILHTDSRT 202
QY 280 CTASTQSC---NDLCEHFCV-----PNDPQGS----- 304
DB 203 C--AINSCALNGGCGHHCVOQLTTRHRCQCRPGQLQEDGHCVRKSPCANRNGSCMR 260
QY 305 -----YSCMCTGYRLADQHRCEVDVDCILBSPPCORCVNTQGFECHCYPNYDL- 356
DB 261 CQVVRGLARCECHVGQYLAADGKACEDVDECAAGLAQCAHGLNTQGSFKVCYCHAGYELG 320
QY 357 VDG-EC---VEPVDPCEFRAN--CEYOCQPLNQTSY--LCVCAEGFAPIPHEPH--RCQM 405
DB 321 ADGRQCYRIEMBIIVNSCEANNNGCSHGC---SHTSAGPLCTCPRGYELDTDQRTICRCR 377
QY 406 FCNQTACPADDDPNTQA--SCECPBEGYILD-DGFTCTDIDECENG-GFGSGVCHNLPGTFE 462
DB 378 LCRQPVLOQVCTNNNGYEGCGYAGYRLSADGCGCEDVDECASSRGGCGHHCTNLAGSFQ 437
QY 463 CIC 465
DB 438 CSC 440

RESULT 15
US-10-453-372-878

; Sequence 878, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:

; APPLICANT: Alsbodrok, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: Curaseqelist version 0.1
; SEQ ID NO 878
; LENGTH: 1403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-878

Query Match 11.8%; Score 379.5; DB 6; Length 1403;
Best Local Similarity 32.3%; Pred. No. 2.1e-19;
Matches 98; Conservative 31; Mismatches 105; Indels 69; Gaps 16;

QY 224 CTAPGAVQ---GHWAEAPGAMDCSVNGGCEHACNAIPGARPCQCPAGAAALQADGRS 279
DB 146 CRWPPSHQLOGDGETCODVD---ECRTHNGGCGHRCVNTPGSYLCECKPGFRILHTDSRT 202
QY 280 CTASTQSC---NDLCEHFCV-----PNDPQGS----- 304
DB 203 C--AINSCALNGGCGHHCVOQLTTRHRCQCRPGQLQEDGHCVRKSPCANRNGSCMR 260
QY 305 -----YSCMCTGYRLADQHRCEVDVDCILBSPPCORCVNTQGFECHCYPNYDL- 356
DB 261 CQVVRGLARCECHVGQYLAADGKACEDVDECAAGLAQCAHGLNTQGSFKVCYCHAGYELG 320
QY 357 VDG-EC---VEPVDPCEFRAN--CEYOCQPLNQTSY--LCVCAEGFAPIPHEPH--RCQM 405
DB 321 ADGRQCYRIEMBIIVNSCEANNNGCSHGC---SHTSAGPLCTCPRGYELDTDQRTICRCR 377
QY 406 FCNQTACPADDDPNTQA--SCECPBEGYILD-DGFTCTDIDECENG-GFGSGVCHNLPGTFE 462
DB 378 LCRQPVLOQVCTNNNGYEGCGYAGYRLSADGCGCEDVDECASSRGGCGHHCTNLAGSFQ 437
QY 463 CIC 465
DB 438 CSC 440

Search completed: February 4, 2006, 04:48:27
Job time : 18 secs

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 4, 2006, 04:44:33 ; Search time 181 Seconds
(without alignments)
1325.050 Million cell updates/sec

Title: US-10-725-013-2
Perfect score: 3203
Sequence: 1 MLGVLVIGALALAGLGFPPAP.....APSKVVLQHVRTERTPQRL 574

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBSCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBSCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBSCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBSCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3203	100.0	574	4	US-10-725-013-2
2	3176.5	99.2	575	4	US-10-150-440-3
3	3176.5	99.2	575	4	US-10-373-801-29
4	3176.5	99.2	575	4	US-10-712-124-110
5	3176.5	99.2	575	5	US-10-785-156-2
6	3176.5	99.2	631	4	US-10-150-440-1
7	3176.5	99.2	631	4	US-10-741-601-309
8	3172.5	99.0	575	3	US-09-938-405-2
9	3172.5	99.0	575	4	US-10-438-648-2
10	3172.5	99.0	575	4	US-10-410-195-2
11	3159.5	98.6	575	4	US-10-094-886-196
12	2789.5	87.1	497	4	US-10-298-796-4
13	1323	41.3	239	4	US-10-104-047-2759
14	1219	38.1	224	5	US-10-478-360-1
15	869	27.1	157	5	US-10-478-360-2
16	792.5	24.7	223	3	US-10-478-360-13
17	775.5	24.2	418	4	US-10-427-805-2
18	753	23.5	397	4	US-10-427-805-3
19	695	21.7	127	5	US-10-478-360-4
20	590.5	18.4	645	4	US-10-029-386-3151
21	590.5	18.4	652	4	US-10-408-765A-1422
22	590.5	18.4	652	5	US-10-741-600-1310
23	590.5	18.4	652	5	US-10-741-600-1311
24	590.5	18.4	652	5	US-10-820-155-1
25	590.5	18.4	652	5	US-10-820-155-79
26	588.5	18.4	652	3	US-09-789-919-96
27	587.5	18.3	648	5	US-10-461-862-116

28	587.5	18.3	648	5	US-10-461-862-118	Sequence 118, App
29	587.5	18.3	652	4	US-10-021-660-83	Sequence 83, App
30	587.5	18.3	652	4	US-10-211-462-131	Sequence 131, App
31	587.5	18.3	652	5	US-10-820-155-82	Sequence 82, App
32	587.5	18.3	652	5	US-10-820-155-117	Sequence 117, App
33	578	18.0	467	4	US-10-210-172-176	Sequence 176, App
34	578	18.0	757	3	US-09-918-715-177	Sequence 177, App
35	578	18.0	757	3	US-09-918-715-196	Sequence 196, App
36	578	18.0	757	4	US-10-262-445-107	Sequence 107, App
37	578	18.0	757	4	US-10-712-124-102	Sequence 102, App
38	578	18.0	757	4	US-10-474-794-177	Sequence 177, App
39	578	18.0	757	4	US-10-474-794-196	Sequence 196, App
40	578	18.0	757	5	US-10-723-860-443	Sequence 443, App
41	578	18.0	757	5	US-10-979-159-177	Sequence 177, App
42	578	18.0	757	5	US-10-979-159-196	Sequence 196, App
43	575	18.0	765	3	US-09-918-715-190	Sequence 190, App
44	575	18.0	765	3	US-09-918-715-291	Sequence 291, App
45	575	18.0	765	4	US-10-474-794-190	Sequence 190, App

ALIGNMENTS

RESULT 1
US-10-725-013-2
; Sequence 2, Application US/10725013
; Publication No. US20040196683A1
; GENERAL INFORMATION:
; APPLICANT: Sehgal, Lakshman R.
; TITLE OF INVENTION: Ex vivo and in vivo expression of the thrombomodulin gene
; FILE REFERENCE: 3840-005-27
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/430,099
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-725-013-2

Query Match	Score	DB 4	Length	574
Best Local Similarity	100.0%	Pred. No. 1.1e-209		
Matches	574	Conservative	0	Mismatches 0; Indels 0; Gaps 0;
QY	1	MLGVLVIGALALAGLGFPPAPPEPOGSGQVCHOCFALYRGPATFLNNSQICDGLRGHLM	60	
DB	1	MLGVLVIGALALAGLGFPPAPPEPOGSGQVCHOCFALYRGPATFLNNSQICDGLRGHLM	60	
QY	61	TVRSVADVLSLLINGDGVGRRRLTWIGLQLPCCGDKRLGPRGFOWTGDNNTSYS	120	
DB	61	TVRSVADVLSLLINGDGVGRRRLTWIGLQLPCCGDKRLGPRGFOWTGDNNTSYS	120	
QY	121	FWARLDLNGALICGFLCAVSAEAETVPSRIWEQCEVYADGFLCEFHFPATREPLAV	180	
DB	121	FWARLDLNGALICGFLCAVSAEAETVPSRIWEQCEVYADGFLCEFHFPATREPLAV	180	
QY	181	EPGAAAASVSTTYGPFPAAGADFOALPVGSSAAVAPLGLQLMCTAPGAVQGHAREAP	240	
DB	181	EPGAAAASVSTTYGPFPAAGADFOALPVGSSAAVAPLGLQLMCTAPGAVQGHAREAP	240	
QY	241	GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSCCTASTQSCNDLCEHFCVPPND	300	
DB	241	GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSCCTASTQSCNDLCEHFCVPPND	300	
QY	301	QPGSYSCMCEYGRILADQHCEDVDICILPSPCPQACVNTQSGFBCHCYPTNDLVNDE	360	
DB	301	QPGSYSCMCEYGRILADQHCEDVDICILPSPCPQACVNTQSGFBCHCYPTNDLVNDE	360	

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Qy 361 CVEBVDPCFRANCEYQCQPLNQTSTYLCVCAEGFAP1PHEPHRCOMFCNQTACPADCDPNT 420
Db 361 CVEBVDPCFRANCEYQCQPLNQTSTYLCVCAEGFAP1PHEPHRCOMFCNQTACPADCDPNT 420
Qy 421 QASCECEBGTYLLDGFICTDIDECENGGFCSGVCHNLPGTFECTICGPDLSALARIHTGTD 480
Db 421 QASCECEBGTYLLDGFICTDIDECENGGFCSGVCHNLPGTFECTICGPDLSALARIHTGTD 480
Qy 481 SGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLRK 540
Db 481 SGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLRK 540
Qy 541 KOGAARAMEYKCAAPSKEVVLQHVTRTERTPORL 574
Db 541 KOGAARAMEYKCAAPSKEVVLQHVTRTERTPORL 574

RESULT 2
US-10-150-440-3
; Sequence 3, Application US/10150440
; Publication No. US2003002249A1
; GENERAL INFORMATION:
; APPLICANT: Schmitz, Uergen
; APPLICANT: Dzlonek, Andrzej
; APPLICANT: Bzloniek, David William
; TITLE OF INVENTION: ANTIGEN-BINDING FRAGMENTS THAT RECOGNIZE
; FILE REFERENCE: 212302001200
; CURRENT FILING DATE: US/10/150,440
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/714,712
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/291,561
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/197,205
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/196,824
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/180,775
; PRIOR FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: US 60/179,003
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/167,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/165,555
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-150-440-3

Query Match 99.2%; Score 3176.5; DB 4; Length 575;
Best Local Similarity 99.5%; Pred. No. 7.1e-208;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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Qy 241 GAMDCSVENGCCEHACNA1PGAPRCQCPAGALQADGSCCTAS-TQSCNDLCEHFCEVNP 299
Db 241 GAMDCSVENGCCEHACNA1PGAPRCQCPAGALQADGSCCTAS-TQSCNDLCEHFCEVNP 300
Qy 300 DQGSYSCEMCEGYRLAADQRCEDVDDCIIEPSPCPCRCVNTQGFECCHCYPNYDLYDG 359
Db 301 DQGSYSCEMCEGYRLAADQRCEDVDDCIIEPSPCPCRCVNTQGFECCHCYPNYDLYDG 360
Qy 360 ECEBVDPCFRANCEYQCQPLNQTSTYLCVCAEGFAP1PHEPHRCOMFCNQTACPADCDPNT 419
Db 361 ECEBVDPCFRANCEYQCQPLNQTSTYLCVCAEGFAP1PHEPHRCOMFCNQTACPADCDPNT 420
Qy 420 TQASCECEBGTYLLDGFICTDIDECENGGFCSGVCHNLPGTFECTICGPDLSALARIHTGTD 479
Db 421 TQASCECEBGTYLLDGFICTDIDECENGGFCSGVCHNLPGTFECTICGPDLSALARIHTGTD 480
Qy 480 DSGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLRK 539
Db 481 DSGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLRK 540
Qy 540 KOGAARAMEYKCAAPSKEVVLQHVTRTERTPORL 574
Db 541 KOGAARAMEYKCAAPSKEVVLQHVTRTERTPORL 575

RESULT 3
US-10-373-801-29
; Sequence 29, Application US/10373801
; Publication No. US2004000564A1
; GENERAL INFORMATION:
; APPLICANT: Yibai Pharmaceutical (USA)
; FILE REFERENCE: 12399.00
; TITLE OF INVENTION: Method and composition for detection and treatment of breast can
; CURRENT FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-373-801-29

Query Match 99.2%; Score 3176.5; DB 4; Length 575;
Best Local Similarity 99.5%; Pred. No. 7.1e-208;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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Db 361 ECVEVDVDCFRANCCYCCQPLNQTSTYLCVCAEGFAPITHEBPRCQPCNQTA CPADCPN 420
Qy 420 TQASCECEGYTLDDGFICTDIDECENGFCGVCCHNPGTFECICGPDALARIHIGTDC 479
Db 421 TQASCECEGYTLDDGFICTDIDECENGFCGVCCHNPGTFECICGPDALARIHIGTDC 480
Qy 480 DSGKVDGSDSGGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
Db 481 DSGKVDGSDSGGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540
Qy 540 KKQGAARAKMEYKCAAPSKVVLQHVTERTPORL 574
Db 541 KKQGAARAKMEYKCAAPSKVVLQHVTERTPORL 575

RESULT 4
US-10-712-124-110
; Sequence 110, Application US/10712124
; Publication No. US20040146907A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, VICTORIA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING DYSPLASIA
; FILE REFERENCE: P2000R1
; CURRENT APPLICATION NUMBER: US/10/712,124
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/425,813
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 110
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-712-124-110

Query Match 99.2%; Score 3176.5; DB 4; Length 575;
Best Local Similarity 99.5%; Pred. No. 7.1e-208;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 MLGTVLVGALALAGLGPAPAPBPQSGSQCVENHDFALYPPGATFLNASQICDGLRGHLM 60
Db 1 MLGTVLVGALALAGLGPAPAPBPQSGSQCVENHDFALYPPGATFLNASQICDGLRGHLM 60
Qy 61 TRSSVADVSTSLINGDGVGRRRLWIGLQLPFGCGDPKRLGRLRGFWMTGDNNTSYS 120
Db 61 TRSSVADVSTSLINGDGVGRRRLWIGLQLPFGCGDPKRLGRLRGFWMTGDNNTSYS 120
Qy 121 RMARLDLNGAPLCPGLCVAVSAEAATVPSBPIMEBQCEVADGFLCEFHFPATCRPLAV 180
Db 121 RMARLDLNGAPLCPGLCVAVSAEAATVPSBPIMEBQCEVADGFLCEFHFPATCRPLAV 180
Qy 181 EPGAAAAVSTTYGTPPARGADFOALPVGSSAAVAPLGLQIMCTAPPGA VQGHARAP 240
Db 181 EPGAAAAVSTTYGTPPARGADFOALPVGSSAAVAPLGLQIMCTAPPGA VQGHARAP 240
Qy 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSCITAS--TOSCNDCI:CEHFCVNP 299
Db 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSCITAS--TOSCNDCI:CEHFCVNP 300
Qy 300 DQPGSYSCMCTGYRLAADQHRCEVDVDCILEPSPCQRCVNTQGFECCHCYPNYDLVDG 359
Db 301 DQPGSYSCMCTGYRLAADQHRCEVDVDCILEPSPCQRCVNTQGFECCHCYPNYDLVDG 360
Qy 360 ECVEPVDPCFRANCCYCCQPLNQTSTYLCVCAEGFAPITHEBPRCQPCNQTA CPADCPN 419
Db 361 ECVEPVDPCFRANCCYCCQPLNQTSTYLCVCAEGFAPITHEBPRCQPCNQTA CPADCPN 420
Qy 420 TQASCECEGYTLDDGFICTDIDECENGFCGVCCHNPGTFECICGPDALARIHIGTDC 479
Db 421 TQASCECEGYTLDDGFICTDIDECENGFCGVCCHNPGTFECICGPDALARIHIGTDC 480
Qy 480 DSGKVDGSDSGGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
Db 481 DSGKVDGSDSGGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540

Db 481 DSGKVDGSDSGGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540
Qy 540 KKQGAARAKMEYKCAAPSKVVLQHVTERTPORL 574
Db 541 KKQGAARAKMEYKCAAPSKVVLQHVTERTPORL 575

RESULT 5
US-10-785-156-2
; Sequence 2, Application US/10785156
; Publication No. US20050106124A1
; GENERAL INFORMATION:
; APPLICANT: Sehgal, Lakshman R.
; APPLICANT: Wong, Jonathan
; APPLICANT: Seth, Prem
; TITLE OF INVENTION: Therapeutic Applications of Thrombomodulin Gene Via Viral and
; TITLE OF INVENTION: Non-viral Vectors
; FILE REFERENCE: 3840-006-27
; CURRENT APPLICATION NUMBER: US/10/785,156
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 60/449,408
; PRIOR FILING DATE: 2003-02-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-785-156-2

Query Match 99.2%; Score 3176.5; DB 5; Length 575;
Best Local Similarity 99.5%; Pred. No. 7.1e-208;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 MLGTVLVGALALAGLGPAPAPBPQSGSQCVENHDFALYPPGATFLNASQICDGLRGHLM 60
Db 1 MLGTVLVGALALAGLGPAPAPBPQSGSQCVENHDFALYPPGATFLNASQICDGLRGHLM 60
Qy 61 TRSSVADVSTSLINGDGVGRRRLWIGLQLPFGCGDPKRLGRLRGFWMTGDNNTSYS 120
Db 61 TRSSVADVSTSLINGDGVGRRRLWIGLQLPFGCGDPKRLGRLRGFWMTGDNNTSYS 120
Qy 121 RMARLDLNGAPLCPGLCVAVSAEAATVPSBPIMEBQCEVADGFLCEFHFPATCRPLAV 180
Db 121 RMARLDLNGAPLCPGLCVAVSAEAATVPSBPIMEBQCEVADGFLCEFHFPATCRPLAV 180
Qy 181 EPGAAAAVSTTYGTPPARGADFOALPVGSSAAVAPLGLQIMCTAPPGA VQGHARAP 240
Db 181 EPGAAAAVSTTYGTPPARGADFOALPVGSSAAVAPLGLQIMCTAPPGA VQGHARAP 240
Qy 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSCITAS--TOSCNDCI:CEHFCVNP 299
Db 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSCITAS--TOSCNDCI:CEHFCVNP 300
Qy 300 DQPGSYSCMCTGYRLAADQHRCEVDVDCILEPSPCQRCVNTQGFECCHCYPNYDLVDG 359
Db 301 DQPGSYSCMCTGYRLAADQHRCEVDVDCILEPSPCQRCVNTQGFECCHCYPNYDLVDG 360
Qy 360 ECVEPVDPCFRANCCYCCQPLNQTSTYLCVCAEGFAPITHEBPRCQPCNQTA CPADCPN 419
Db 361 ECVEPVDPCFRANCCYCCQPLNQTSTYLCVCAEGFAPITHEBPRCQPCNQTA CPADCPN 420
Qy 420 TQASCECEGYTLDDGFICTDIDECENGFCGVCCHNPGTFECICGPDALARIHIGTDC 479
Db 421 TQASCECEGYTLDDGFICTDIDECENGFCGVCCHNPGTFECICGPDALARIHIGTDC 480
Qy 480 DSGKVDGSDSGGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
Db 481 DSGKVDGSDSGGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540
Qy 540 KKQGAARAKMEYKCAAPSKVVLQHVTERTPORL 574
Db 541 KKQGAARAKMEYKCAAPSKVVLQHVTERTPORL 575

```
RESULT 6
US-10-150-440-1
; Sequence 1, Application US/10150440
; Publication No. US2003022249A1
; GENERAL INFORMATION:
; APPLICANT: Schmitz, Ueergen
; APPLICANT: Schmitz, Andrej
; APPLICANT: Dzionek, William
; APPLICANT: Buck, David William
; TITLE OF INVENTION: ANTIGEN-BINDING FRAGMENTS THAT RECOGNIZE
; TITLE OF INVENTION: A SUBSET OF DENDRITIC CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: 212302001200
; CURRENT APPLICATION NUMBER: US/10/150.440
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/714,712
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/291,561
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/197,205
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/196,824
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/180,775
; PRIOR FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: US 60/179,003
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/167,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/165,555
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-150-440-1

Query Match      99.2%; Score 3176.5; DB 4; Length 631;
Best Local Similarity 99.5%; Pred. No. 7.8e-208;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      1  MLGVLVGLALALAGLPAPAPAPPOGSGSCVCHDCEPALYPGPATFLNASQICDGLRGHLM 60
DB      57  MLGVLVGLALALAGLPAPAPAPPOGSGSCVCHDCEPALYPGPATFLNASQICDGLRGHLM 116
QY      61  TYRSSVAADVLSLLINGDGVGRRRLWIGLQLPPGCGDPKRLGRLGFQWVTGDNNTSYS 120
DB      117  TYRSSVAADVLSLLINGDGVGRRRLWIGLQLPPGCGDPKRLGRLGFQWVTGDNNTSYS 176
QY      121  RWARLDLNGAPLCGPLCVAVSAAEATVPSEPIWEEQCEVADGFLCEHFHPATCRPLAV 180
DB      177  RWARLDLNGAPLCGPLCVAVSAAEATVPSEPIWEEQCEVADGFLCEHFHPATCRPLAV 236
QY      181  EGGAAAANVSTYGGPFARAGADFOALPYGSSAAVAPLGLQIMCTAPPGAVQGHMAREAP 240
DB      237  EGGAAAANVSTYGGPFARAGADFOALPYGSSAAVAPLGLQIMCTAPPGAVQGHMAREAP 296
QY      241  GAMDCSVENGCGEHCNAIPGARPCQCPAGALQADGRSCTAS-TOSCNDLCEHFCVNP 299
DB      297  GAMDCSVENGCGEHCNAIPGARPCQCPAGALQADGRSCTASATOSCNDLCEHFCVNP 356
QY      300  DPGSGYSWCETGYRLADQHRCEVDVDCILBSPCPQRCVNTQGGFCHCYPNTDLYDG 359
DB      357  DPGSGYSWCETGYRLADQHRCEVDVDCILBSPCPQRCVNTQGGFCHCYPNTDLYDG 416
QY      360  ECVPEVDPFRANCERYQOCPINOTSYLTCVABGFAPIPHEPHRCOMFCNQTACPADCDN 419
DB      417  ECVPEVDPFRANCERYQOCPINOTSYLTCVABGFAPIPHEPHRCOMFCNQTACPADCDN 476
QY      420  TQASCECPBGYILDDGFICTDIDECENGFGSGVCHNLPGTFECICGPDALARRHIGTDC 479
DB      479  TQASCECPBGYILDDGFICTDIDECENGFGSGVCHNLPGTFECICGPDALARRHIGTDC 536
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US-10-741-601-309
; Sequence 309, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001500
; CURRENT APPLICATION NUMBER: US/10/741.601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 309
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-309

Query Match      99.2%; Score 3176.5; DB 4; Length 631;
Best Local Similarity 99.5%; Pred. No. 7.8e-208;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      1  MLGVLVGLALALAGLPAPAPAPPOGSGSCVCHDCEPALYPGPATFLNASQICDGLRGHLM 60
DB      57  MLGVLVGLALALAGLPAPAPAPPOGSGSCVCHDCEPALYPGPATFLNASQICDGLRGHLM 116
QY      61  TYRSSVAADVLSLLINGDGVGRRRLWIGLQLPPGCGDPKRLGRLGFQWVTGDNNTSYS 120
DB      117  TYRSSVAADVLSLLINGDGVGRRRLWIGLQLPPGCGDPKRLGRLGFQWVTGDNNTSYS 176
QY      121  RWARLDLNGAPLCGPLCVAVSAAEATVPSEPIWEEQCEVADGFLCEHFHPATCRPLAV 180
DB      177  RWARLDLNGAPLCGPLCVAVSAAEATVPSEPIWEEQCEVADGFLCEHFHPATCRPLAV 236
QY      181  EGGAAAANVSTYGGPFARAGADFOALPYGSSAAVAPLGLQIMCTAPPGAVQGHMAREAP 240
DB      237  EGGAAAANVSTYGGPFARAGADFOALPYGSSAAVAPLGLQIMCTAPPGAVQGHMAREAP 296
QY      241  GAMDCSVENGCGEHCNAIPGARPCQCPAGALQADGRSCTAS-TOSCNDLCEHFCVNP 299
DB      297  GAMDCSVENGCGEHCNAIPGARPCQCPAGALQADGRSCTASATOSCNDLCEHFCVNP 356
QY      300  DPGSGYSWCETGYRLADQHRCEVDVDCILBSPCPQRCVNTQGGFCHCYPNTDLYDG 359
DB      357  DPGSGYSWCETGYRLADQHRCEVDVDCILBSPCPQRCVNTQGGFCHCYPNTDLYDG 416
QY      360  ECVPEVDPFRANCERYQOCPINOTSYLTCVABGFAPIPHEPHRCOMFCNQTACPADCDN 419
DB      417  ECVPEVDPFRANCERYQOCPINOTSYLTCVABGFAPIPHEPHRCOMFCNQTACPADCDN 476
QY      420  TQASCECPBGYILDDGFICTDIDECENGFGSGVCHNLPGTFECICGPDALARRHIGTDC 479
DB      479  TQASCECPBGYILDDGFICTDIDECENGFGSGVCHNLPGTFECICGPDALARRHIGTDC 536
QY      480  DSGKVDGDSGSGBPSPPTPGSTLTPPAVLVHSGLLIGISTASLCLVALLALLCHLR 539
DB      537  DSGKVDGDSGSGBPSPPTPGSTLTPPAVLVHSGLLIGISTASLCLVALLALLCHLR 596
QY      540  KQGAARAKMEYKCAAPSKVVLQHVTERTPQRL 574
DB      597  KQGAARAKMEYKCAAPSKVVLQHVTERTPQRL 631
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RESULT 8
US-09-938-405-2
; Sequence 2, Application US/09938405
; Patent No. US2002011296A1
; GENERAL INFORMATION:
; APPLICANT: Festoff, Barry W.
; APPLICANT: Morser, Michael J.
; TITLE OF INVENTION: Thrombomodulin Analogs for Use in Recovery of Spinal Cord Injury
; FILE REFERENCE: 51960AUSM1
; CURRENT APPLICATION NUMBER: US/09/938,405
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 60/229,714
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-405-2

Query Match          99.0%; Score 3172.5; DB 3; Length 575;
Best Local Similarity 99.3%; Pred. No. 1.3e-207;
Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MGVTVLGAALAGAGFPAPAPAPPOGSGQCVHDCFFALYPGPATFLNLSQICDGLRGHLM 60
DB 1 MGVTVLGAALAGAGFPAPAPAPPOGSGQCVHDCFFALYPGPATFLNLSQICDGLRGHLM 60
QY 61 TVRSSVAADVLSILNGDGVGRRRLMTGLQLPFCGCBPKRLGRLRGFWTGDNNNTSYS 120
DB 61 TVRSSVAADVLSILNGDGVGRRRLMTGLQLPFCGCBPKRLGRLRGFWTGDNNNTSYS 120
QY 121 RWARLDLNGALICGLPCVAVAASAEATVSEPIWEEOCEVADGFLCEFHFPATCRPLAV 180
DB 121 RWARLDLNGALICGLPCVAVAASAEATVSEPIWEEOCEVADGFLCEFHFPATCRPLAV 180
QY 181 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPGAAGVGHAREAP 240
DB 181 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPGAAGVGHAREAP 240
QY 241 GAMDCSVNGGCEHACNAIPGARPCQCPAGALQADGSSCTAS-TQSCNDLCEHFCVNP 299
DB 241 GAMDCSVNGGCEHACNAIPGARPCQCPAGALQADGSSCTAS-TQSCNDLCEHFCVNP 299
QY 300 DOPGYSVCMECTGYRLADQHRCEVDVDDCILEPSPCPCPCVNTQGFECCHCYPNYDLVDG 359
DB 300 DOPGYSVCMECTGYRLADQHRCEVDVDDCILEPSPCPCPCVNTQGFECCHCYPNYDLVDG 359
QY 360 ECEVPVDCFRANCEYQCPINQTSYLCVCAEGFAPIPHEBRCQMFNCQTAACPADCPN 419
DB 360 ECEVPVDCFRANCEYQCPINQTSYLCVCAEGFAPIPHEBRCQMFNCQTAACPADCPN 419
QY 420 TQASCECEBEGYILDDGFLCTDIDECENGFGSGVCCHNPGTFECCICGDSALARIITGDC 479
DB 420 TQASCECEBEGYILDDGFLCTDIDECENGFGSGVCCHNPGTFECCICGDSALARIITGDC 479
QY 480 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCILR 539
DB 480 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCILR 539
QY 540 KKQGAARAKMEYKCAAPSEKVVLOHVRTERTPORL 574
DB 540 KKQGAARAKMEYKCAAPSEKVVLOHVRTERTPORL 574
; RESULT 9
US-10-438-648-2
; Sequence 2, Application US/10438648
; Publication No. US2003018683A1
; GENERAL INFORMATION:
; APPLICANT: Festoff, Barry W.
; APPLICANT: Morser, Michael J.
; TITLE OF INVENTION: Thrombomodulin Analogs for Use in Recovery of Spinal Cord Injury
; FILE REFERENCE: 51960AUSM1
```

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; APPLICANT: Light, David
; APPLICANT: Nagashima, Mariko
; APPLICANT: Morser, Michael J.
; TITLE OF INVENTION: Thrombomodulin Analogs for Pharmaceutical Use
; FILE REFERENCE: 51863AUSD1
; CURRENT APPLICATION NUMBER: US/10/438,648
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US 60/213,678
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 09/880,484
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-438-648-2

Query Match          99.0%; Score 3172.5; DB 4; Length 575;
Best Local Similarity 99.3%; Pred. No. 1.3e-207;
Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MGVTVLGAALAGAGFPAPAPAPPOGSGQCVHDCFFALYPGPATFLNLSQICDGLRGHLM 60
DB 1 MGVTVLGAALAGAGFPAPAPAPPOGSGQCVHDCFFALYPGPATFLNLSQICDGLRGHLM 60
QY 61 TVRSSVAADVLSILNGDGVGRRRLMTGLQLPFCGCBPKRLGRLRGFWTGDNNNTSYS 120
DB 61 TVRSSVAADVLSILNGDGVGRRRLMTGLQLPFCGCBPKRLGRLRGFWTGDNNNTSYS 120
QY 121 RWARLDLNGALICGLPCVAVAASAEATVSEPIWEEOCEVADGFLCEFHFPATCRPLAV 180
DB 121 RWARLDLNGALICGLPCVAVAASAEATVSEPIWEEOCEVADGFLCEFHFPATCRPLAV 180
QY 181 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPGAAGVGHAREAP 240
DB 181 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPGAAGVGHAREAP 240
QY 241 GAMDCSVNGGCEHACNAIPGARPCQCPAGALQADGSSCTAS-TQSCNDLCEHFCVNP 299
DB 241 GAMDCSVNGGCEHACNAIPGARPCQCPAGALQADGSSCTAS-TQSCNDLCEHFCVNP 299
QY 300 DOPGYSVCMECTGYRLADQHRCEVDVDDCILEPSPCPCPCVNTQGFECCHCYPNYDLVDG 359
DB 300 DOPGYSVCMECTGYRLADQHRCEVDVDDCILEPSPCPCPCVNTQGFECCHCYPNYDLVDG 359
QY 360 ECEVPVDCFRANCEYQCPINQTSYLCVCAEGFAPIPHEBRCQMFNCQTAACPADCPN 419
DB 360 ECEVPVDCFRANCEYQCPINQTSYLCVCAEGFAPIPHEBRCQMFNCQTAACPADCPN 419
QY 420 TQASCECEBEGYILDDGFLCTDIDECENGFGSGVCCHNPGTFECCICGDSALARIITGDC 479
DB 420 TQASCECEBEGYILDDGFLCTDIDECENGFGSGVCCHNPGTFECCICGDSALARIITGDC 479
QY 480 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCILR 539
DB 480 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCILR 539
QY 540 KKQGAARAKMEYKCAAPSEKVVLOHVRTERTPORL 574
DB 540 KKQGAARAKMEYKCAAPSEKVVLOHVRTERTPORL 574
; RESULT 10
US-10-410-195-2
; Sequence 2, Application US/10410195
; Publication No. US20040002446A1
; GENERAL INFORMATION:
; APPLICANT: Festoff, Barry W.
; APPLICANT: Morser, Michael J.
; TITLE OF INVENTION: Thrombomodulin Analogs for Use in Recovery of Spinal Cord Injury
; FILE REFERENCE: 51960AUSM1
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; CURRENT APPLICATION NUMBER: US/10/410.195
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US/09/938, 405
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 60/229, 714
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent version 3.1
; SEQ ID NO 2
; LENGTH: 575
; TYPE: PRY
; ORGANISM: Homo sapiens
US-10-410-195-2

Query Match      99.0%; Score 3172.5; DB 4; Length 575;
Best Local Similarity 99.3%; Pred. No. 1.3e-207;
Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY      1  MLGVLVIGALALAGLGFPAAPAEPPQSGSQVCHDCFPALYPGPATFLNASQICDGLRGHLM 60
DB      1  MLGVLVIGALALAGLGFPAAPAEPPQSGSQVCHDCFPALYPGPATFLNASQICDGLRGHLM 60
QY      61  TYRSSVAADVSTLLANGGGVGRRLMTGLQLPFGCGPKRLGRLRGFWTGDNNTSYS 120
DB      61  TYRSSVAADVSTLLANGGGVGRRLMTGLQLPFGCGPKRLGRLRGFWTGDNNTSYS 120
QY      121  RWARLDLNGAPLCGFLCYAVASAATVPSEPIWEEOQCEVADGFLCFHFPPATCRPLAY 180
DB      121  RWARLDLNGAPLCGFLCYAVASAATVPSEPIWEEOQCEVADGFLCFHFPPATCRPLAY 180
QY      181  BPGAAAAVSTITGTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPGAVOGHWAREAP 240
DB      181  BPGAAAAVSTITGTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPGAVOGHWAREAP 240
QY      241  GAMDCSVENGSGCEHACNAIPGARPCQCPAGALQADGRCTAS-TQSCNDLCENHCVPNP 299
DB      241  GAMDCSVENGSGCEHACNAIPGARPCQCPAGALQADGRCTAS-TQSCNDLCENHCVPNP 299
QY      300  DOPGYSVCMTGTYTLADQHRCEVDDCITLPSPCQPCVNTQGGFECGCPNTDLYDG 359
DB      301  DOPGYSVCMTGTYTLADQHRCEVDDCITLPSPCQPCVNTQGGFECGCPNTDLYDG 360
QY      360  ECVEVDPCFRANCEYQCOPLNQTSLCYCAGFAPIPHEPRCOMFCNQTACPADCDPN 419
DB      361  ECVEVDPCFRANCEYQCOPLNQTSLCYCAGFAPIPHEPRCOMFCNQTACPADCDPN 420
QY      420  TQASCECEBGTYLIDGFTCTDIDECENGFGCGVCHNLPGTEECTCGPSALARRITGDC 479
DB      421  TQASCECEBGTYLIDGFTCTDIDECENGFGCGVCHNLPGTEECTCGPSALARRITGDC 480
QY      480  DSGKVDGGSGSGEPSPPTPGSTLTTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
DB      481  DSGKVDGGSGSGEPSPPTPGSTLTTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540
QY      540  KKOGAARAMEYKCAAPSKKVVLOHVRTERTPQRL 574
DB      541  KKOGAARAMEYKCAAPSKKVVLOHVRTERTPQRL 575

RESULT 11
US-10-094-886-196
; Sequence 196, Application US/10094886
; Publication No. US20040002120A1
; GENERAL INFORMATION:
; APPLICANT: Kerkhev, Ramesh
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Paturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Vernet, Corinne A.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda

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; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Taubier, Raymond J., Jr.
; APPLICANT: Miller, Charles
; APPLICANT: Caeman, Stacie
; APPLICANT: Pena, Carol
; APPLICANT: Gangoli, Esna
; APPLICANT: Gusev, Vladimir
; APPLICANT: Smithson, Glenda
; APPLICANT: Zernhusen, Bryan
; APPLICANT: Gerlach, Valerie
; APPLICANT: Pochart, Pascal
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkors, Richard
; APPLICANT: Raetelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Larochele, William
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-290 B
; CURRENT APPLICATION NUMBER: US/10/094, 886
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274, 322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313, 182
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/288, 052
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/318, 510
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/274, 281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/314, 018
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/274, 194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274, 849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/296, 693
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/313, 626
; PRIOR FILING DATE: 2001-08-21
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: Patent in 2.1
; SEQ ID NO 196
; LENGTH: 575
; TYPE: PRY
; ORGANISM: Homo sapiens
US-10-094-886-196

Query Match      98.6%; Score 3159.5; DB 4; Length 575;
Best Local Similarity 99.0%; Pred. No. 1e-206;
Matches 569; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY      1  MLGVLVIGALALAGLGFPAAPAEPPQSGSQVCHDCFPALYPGPATFLNASQICDGLRGHLM 60
DB      1  MLGVLVIGALALAGLGFPAAPAEPPQSGSQVCHDCFPALYPGPATFLNASQICDGLRGHLM 60
QY      61  TYRSSVAADVSTLLANGGGVGRRLMTGLQLPFGCGPKRLGRLRGFWTGDNNTSYS 120
DB      61  TYRSSVAADVSTLLANGGGVGRRLMTGLQLPFGCGPKRLGRLRGFWTGDNNTSYS 120
QY      121  RWARLDLNGAPLCGFLCYAVASAATVPSEPIWEEOQCEVADGFLCFHFPPATCRPLAY 180
DB      121  RWARLDLNGAPLCGFLCYAVASAATVPSEPIWEEOQCEVADGFLCFHFPPATCRPLAY 180
QY      181  BPGAAAAVSTITGTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPGAVOGHWAREAP 240
DB      181  BPGAAAAVSTITGTPFAARGADFOALPVGSSAAVAAPLGLQIMCTAPGAVOGHWAREAP 240

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Qy 241 GAMDCEVNGGCEHACNAIPGARPCQCPAGALQADGASCTAS-TOSCNDLCEHFVNP 299
Db 241 GAMDCEVNGGCEHACNAIPGARPCQCPAGALQADGASCTASATOSCNDLCEHFVNP 300
Qy 300 DQPSYSCMCTGYRLADQHRCEVDVDCILBPSPCPCVNTQGGFECHCYPNVDVVG 359
Db 301 DQPSYSCMCTGYRLADQHRCEVDVDCILBPSPCPCVNTQGGFECHCYPNVDVVG 360
Qy 360 ECVBVDPCFRANCERYOCPLNQTSLCYCAGGAPAPIPHEPRCOMFCNQACPADCPN 419
Db 361 ECVBVDPCFRANCERYOCPLNQTSLCYCAGGAPAPIPHEPRCOMFCNQACPADCPN 420
Qy 420 TQASCEBEGYILDDGFICTDIDECENGFGSGVCHNLPGTFECICGPDALARIHIGTDC 479
Db 421 TQASCEBEGYILDDGFICTDIDECENGFGSGVCHNLPGTFECICGPDALARIHIGTDC 480
Qy 480 DSGKYDGDSSGSEPPSPPTGSTLTTPAVGLVHSGLLIGISIASLCLVALLALCHLR 539
Db 481 DSGKYDGDSSGSEPPSPPTGSTLTTPAVGLVHSGLLIGISIASLCLVALLALCHLR 540
Qy 540 KKQGAARAKMEYKCAAPSKVVLQHVTERTPORL 574
Db 541 KKQGAARAKMEYKCAAPSKVVLQHVTERTPORL 575

RESULT 12

US-10-298-796-4
; Sequence 4, Application US/10298796
; Publication No. US2003020490A1
; GENERAL INFORMATION:
; APPLICANT: KURIYAMA, Shinichi
; APPLICANT: HASEGAWA, Takashi
; TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
; FILE REFERENCE: 1110-253P
; CURRENT APPLICATION NUMBER: US/10/298,796
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US/09/331,793
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-298-796-4

Query Match 87.1%; Score 2789.5; DB 4; Length 497;
Best Local Similarity 99.2%; Pred. No. 1.3e-181;
Matches 493; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 19 AAPAPQPGSGSCVHDCFPALYGPATFLINASQICGLRGLHMTYRASSVAADVISILLNGD 78
Db 1 AAPAPQPGSGSCVHDCFPALYGPATFLINASQICGLRGLHMTYRASSVAADVISILLNGD 60
Qy 79 GGVBRRLMIGLQIPPGGDKRLGELRFGQMTVGDNNNTSYRNRRLDNLGAPICGPICV 138
Db 61 GGVBRRLMIGLQIPPGGDKRLGELRFGQMTVGDNNNTSYRNRRLDNLGAPICGPICV 120
Qy 139 AVSAAEATVPSSEPIWEEQCEVKADGFLCEHFPAFCPLAVEPQAAAAVSYTYGTFPA 198
Db 121 AVSAAEATVPSSEPIWEEQCEVKADGFLCEHFPAFCPLAVEPQAAAAVSYTYGTFPA 180
Qy 199 ARGADFOALPYVGSSAAVAPLGIQLMCTAPPGAQVGHMARRAPGAMDCSVENGGEHACNA 258
Db 181 ARGADFOALPYVGSSAAVAPLGIQLMCTAPPGAQVGHMARRAPGAMDCSVENGGEHACNA 240
Qy 259 IRGAPCCCPAGALQADGASCTAS-TOSCNDLCEHFVNPDPDGSYSCMCTGYRLAA 317
Db 241 IRGAPCCCPAGALQADGASCTASATOSCNDLCEHFVNPDPDGSYSCMCTGYRLAA 300
Qy 318 DQHRCEVDVDCILBPSPCPCVNTQGGFECHCYPNVDVGECEVVDPCFRANCERYOC 377
Db 318 DQHRCEVDVDCILBPSPCPCVNTQGGFECHCYPNVDVGECEVVDPCFRANCERYOC 377

Db 301 DQHRCEVDVDCILBPSPCPCVNTQGGFECHCYPNVDVGECEVVDPCFRANCERYOC 360
Qy 378 QPLNQTSLCYCAGGAPAPIPHEPRCOMFCNQACPADCDPNTQASCEBEGYILDDGFI 437
Db 361 QPLNQTSLCYCAGGAPAPIPHEPRCOMFCNQACPADCDPNTQASCEBEGYILDDGFI 420
Qy 438 CTDIDECENGFGSGVCHNLPGTFECICGPDALARIHIGTDCSGKYDGDSSGSEPPSPS 497
Db 421 CTDIDECENGFGSGVCHNLPGTFECICGPDALARIHIGTDCSGKYDGDSSGSEPPSPS 480
Qy 498 PTPGSTLTTPAVGLVHS 514
Db 481 PTPGSTLTTPAVGLVHS 497

RESULT 13

US-10-104-047-2759
; Sequence 2759, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2759
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2759

Query Match 41.3%; Score 1323; DB 4; Length 239;
Best Local Similarity 89.1%; Pred. No. 3.9e-82;
Matches 238; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

Qy 308 MCEYGYRLADQHRCEVDVDCILBPSPCPCVNTQGGFECHCYPNVDVGECEVVDP 367
Db 1 MCEYGYRLADQHRCEVDVDCILBPSPCPCVNTQGGFECHCYPNVDVGECEVVDP 60
Qy 368 CFRANCEYOCPLNQTSLCYCAGGAPAPIPHEPRCOMFCNQACPADCDPNTQASCECP 427
Db 61 CFRANCEYOCPLNQTSLCYCAGGAPAPIPHEPRCOMFCNQACPADCDPNTQASCE-- 118
Qy 428 EGYILDDGFICTDIDECENGFGSGVCHNLPGTFECICGPDALARIHIGTDCSGKYDGG 487
Db 119 -----CHNLPGTFECICGPDALARIHIGTDCSGKYDGG 152
Qy 488 DSGSGSEPPSPPTGSTLTTPAVGLVHSGLLIGISIASLCLVALLALCHLRKKQGAARA 547
Db 153 DSGSGSEPPSPPTGSTLTTPAVGLVHSGLLIGISIASLCLVALLALCHLRKKQGAARA 212
Qy 548 KMEYKCAAPSKVVLQHVTERTPORL 574
Db 213 KMEYKCAAPSKVVLQHVTERTPORL 239

RESULT 14

US-10-478-360-1
; Sequence 1, Application US/10478360
; Publication No. US20050014220A1
; GENERAL INFORMATION:
; APPLICANT: Conway, Edward M.
; TITLE OF INVENTION: THE LECTIN LIKE DOMAIN OF THROMBOMODULIN
; FILE REFERENCE: DECLE70.002APC
; CURRENT APPLICATION NUMBER: US/10/478,360
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/EP02/05727
; PRIOR FILING DATE: 2002-05-24

;; PRIOR APPLICATION NUMBER: EP 01201979.0
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 224
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (1)...(224)
;; OTHER INFORMATION: Human thrombomodulin fragment 1
US-10-478-360-1

Query Match 38.1%; Score 1219; DB 5; Length 224;
Best Local Similarity 100.0%; Pred. No. 4,4e-75;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AEPQGGSCVYHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVISLLINGDGG 80
DB 1 AEPQGGSCVYHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVISLLINGDGG 60
QY 81 VGRRLWIGLQLPFGCGPKRLGRLGFQWTTGDNNTSYSRWRLDNGAPLCGPLCVAV 140
DB 61 VGRRLWIGLQLPFGCGPKRLGRLGFQWTTGDNNTSYSRWRLDNGAPLCGPLCVAV 120
QY 141 SAAEATVPSEPIWEEOCEVADGFLCEFHFPATCRPLAVEPGAAAASITYGTFPAAR 200
DB 121 SAAEATVPSEPIWEEOCEVADGFLCEFHFPATCRPLAVEPGAAAASITYGTFPAAR 180
QY 201 GADFOALPVGSSAAVAPLGLQIMCTAPPAVQGHWAREAPGAMD 244
DB 181 GADFOALPVGSSAAVAPLGLQIMCTAPPAVQGHWAREAPGAMD 224

RESULT 15
US-10-478-360-2
;; Sequence 2, Application US/10478360
;; Publication No. US20050014220A1
;; GENERAL INFORMATION:
;; APPLICANT: Conway, Edward M.
;; TITLE OF INVENTION: THE LECTIN LIKE DOMAIN OF THROMBOMODULIN
;; TITLE OF INVENTION: AND ITS THERAPEUTIC USE
;; FILE REFERENCE: DEC1E70.002APC
;; CURRENT APPLICATION NUMBER: US/10/478,360
;; PRIOR FILING DATE: 2003-11-21
;; PRIOR APPLICATION NUMBER: PCT/EP02/05727
;; PRIOR FILING DATE: 2002-05-24
;; PRIOR APPLICATION NUMBER: EP 01201979.0
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 157
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (1)...(157)
;; OTHER INFORMATION: Human thrombomodulin fragment 2
US-10-478-360-2

Query Match 27.1%; Score 869; DB 5; Length 157;
Best Local Similarity 100.0%; Pred. No. 2e-51;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AEPQGGSCVYHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVISLLINGDGG 80
DB 1 AEPQGGSCVYHDCFALYPGPATFLNASQICDGLRGHLMTVRSSVAADVISLLINGDGG 60
QY 81 VGRRLWIGLQLPFGCGPKRLGRLGFQWTTGDNNTSYSRWRLDNGAPLCGPLCVAV 140
DB 61 VGRRLWIGLQLPFGCGPKRLGRLGFQWTTGDNNTSYSRWRLDNGAPLCGPLCVAV 120

QY 141 SAAEATVPSEPIWEEOCEVADGFLCEFHFPATCRP 177
DB 121 SAAEATVPSEPIWEEOCEVADGFLCEFHFPATCRP 157

Search completed: February 4, 2006, 04:48:04
Job time : 183 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 4, 2006, 04:24:27 ; Search time 199 Seconds

(without alignments)
1267.354 Million cell updates/sec

Title: US-10-725-013-2

Perfect score: 3203
Sequence: 1 MLGVLVIGALALAGLPAP.....APSKENVLQHVTRTEPQRL 574

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*
9: geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3176.5	99.2	575	6	ABG72575 Human chr
2	3176.5	99.2	575	7	ABM78950 Breast ca
3	3176.5	99.2	575	7	ADE54760 Human Pro
4	3176.5	99.2	575	7	ADD48168 Human Pro
5	3176.5	99.2	575	8	ADN04006 Antipsoi
6	3176.5	99.2	575	8	ADP12616 Protein e
7	3176.5	99.2	575	8	ADO28681 Human chr
8	3176.5	99.2	575	8	ADP79506 Human chr
9	3176.5	99.2	575	8	ADR32191 Human chr
10	3176.5	99.2	575	8	ADU06321 Novel bro
11	3176.5	99.2	631	6	ABG72572 Human chr
12	3176.5	99.2	681	6	ADN05602 Antipsoi
13	3172.5	99.0	575	2	AAR11534 Human chr
14	3172.5	99.0	575	2	AAR41806 Thrombo
15	3172.5	99.0	575	2	AAR43031 Human chr
16	3172.5	99.0	575	2	AAR17521 Human chr
17	3172.5	99.0	575	2	AAR23026 Human chr
18	3170.5	99.0	575	1	AAE23026 Human chr
19	3168.5	98.9	575	1	AAE23026 Human chr
20	3163.5	98.6	575	2	AAE23026 Human chr
21	3159.5	98.6	575	2	AAE23026 Human chr
22	3159.5	98.6	575	2	AAE23026 Human chr
23	3139.5	98.0	575	2	AAE23026 Human chr
24	3122.5	97.5	575	2	AAE23026 Human chr

25	3083.5	96.3	557	5	AAE17528 Human chr
26	3083.5	96.3	557	5	AAE17525 Human chr
27	3083.5	96.3	557	5	AAE23031 Human chr
28	3083.5	96.3	557	5	AAE23028 Human chr
29	3082.5	96.2	557	5	AAE17523 Human chr
30	3081.5	96.2	557	5	AAE17596 Human chr
31	3080.5	96.2	557	5	AAE17530 Human chr
32	3080.5	96.2	557	5	AAE17538 Human chr
33	3079.5	96.1	557	5	AAE17526 Human chr
34	3079.5	96.1	557	5	AAE23029 Human chr
35	3078.5	96.1	557	5	AAE17593 Human chr
36	3078.5	96.1	557	5	AAE17595 Human chr
37	3078.5	96.1	557	5	AAE17597 Human chr
38	3078.5	96.1	557	5	AAE17529 Human chr
39	3078.5	96.1	557	5	AAE17527 Human chr
40	3078.5	96.1	557	5	AAE23030 Human chr
41	3077.5	96.1	557	5	AAE17592 Human chr
42	3077.5	96.1	557	5	AAE17594 Human chr
43	3077.5	96.1	557	5	AAE17591 Human chr
44	3076.5	96.1	557	5	AAE17524 Human chr
45	3071.5	95.9	554	5	AAE17522 Human chr

ALIGNMENTS

RESULT 1
ABG72575
ID ABG72575 standard, protein, 575 AA.
AC ABG72575;
DT 05-MAR-2003 (first entry)
DE Human thrombomodulin protein #2 (CD141).
KW Human; thrombomodulin; CD141; dendritic cell separation; inflammation; antiinflammatory; cytostatic; antirheumatic; antithrombotic; cancer; immunosuppressive; dermatological; cell therapy; dermatomyositis; cancer; autoimmune disorder; rheumatoid arthritis; psoriatic arthritis; alkylosing spondylitis; Sjogren's syndrome; lupus erythematosus; Goodpasture's syndrome; scleroderma; vasculitis; polymyositis.
OS Homo sapiens.
XX WO200293172-A1.
XX 21-NOV-2002.
XX 17-MAY-2002; 2002WO-US015786.
XX 17-MAY-2001; 2001US-0291561P.
XX (MILT-) MILTENYI BIOTEC INC.
XX Schmitz J, Dzionek A, Buck DW;
XX WPI; 2003-129324/12.
XX Enriching for dendritic cells from a mixture of cells, useful for treating inflammation, cancer or autoimmune disorders such as arthritis, PT or lupus by contacting the mixture of cell with an antigen-binding fragment specific for CD141.
XX Example 1; Fig 3B; 88pp; English.
XX This invention relates to a novel method for separating dendritic cells from a mixture of cells. The method comprises contacting the mixture of cells with an antigen-binding fragment specific for CD141, and selecting the cells that are CD141 positive therefore producing a dendritic cell-enriched composition. The method of the invention may have immunosuppressive and dermatological activities and may be used in cell

therapy. The methods, compositions and agents of the invention are useful for treating inflammation, cancer or autoimmune disorders such as rheumatoid arthritis, psoriatic arthritis, ankylosing spondylitis, Sjögren's syndrome, lupus erythematosus, Goodpasture's syndrome, scleroderma, vasculitis, polymyositis or dermatomyositis. The dendritic cells and populations are useful for screening assays for agents that affect dendritic cell function, and for the phenotypic, functional, biochemical or molecular analyses of dendritic cells. The compositions and dendritic cells are useful as vaccine adjuvants. The present sequence represents a protein sequence of human CD141 protein which is used to generate the dendritic cell specific antibodies that are used in the method of the invention

SQ Sequence 575 AA;

Query Match	99.2%	Score 3176.5	DB 6	Length 575
Best Local Similarity	99.5%	Pred. No. 6.1e-175		
Matches 572; Conservative	0	Mismatches 2	Indels 1	Gaps 1

OY		1	MIGVIVLGAALAAAGLGFPAPAEPPQGGSGCVDHEDCALTPGATPTPLNASQICGLGHHM	60
Dd		1	MLGVVLGLAALAAAGLGFPAPAEPPQGGSGCVDHEDCALTPGATPTPLNASQICGLGHHM	60
OY		61	TWRSSVAADVITLLINGDGGVGRRRLMIGLQLEPGCGDPKRLGLPFGVNTDDNNTSYS	120
Dd		61	TYRSSVAADVITLLINGDGGVGRRRLMIGLQLEPGCGDPKRLGLPFGVNTDDNNTSYS	120
OY		121	RWARLDLNGABPLCGPLCVAVSAEAATVPSEPIWEEQQCEVKADGPLCEHFHPATCRPLAV	180
Dd		121	RWARLDLNGABPLCGPLCVAVSAEAATVPSEPIWEEQQCEVKADGPLCEHFHPATCRPLAV	180
OY		181	BEGAAAAAVSTTGTGPFAARGADFOLLPVGSMAVAPLGIQLMCTAPRGAVGHMAAREAP	240
Dd		181	BEGAAAAAVSTTGTGPFAARGADFOLLPVGSMAVAPLGIQLMCTAPRGAVGHMAAREAP	240
OY		241	GAMDCSVENGGECHNCNALPGARPCCPGPAALQAQDRSCTAS-TOSCNDLCEHFCEVPNP	299
Dd		241	GAMDCSVENGGECHNCNALPGARPCCPGPAALQAQDRSCTASATOSCNDLCEHFCEVPNP	300
OY		300	DOPGSYSQMCETGYRLAADQHRCEDVDDCILBSPCORCVNTQGFECHCYPNYDLVDG	359
Dd		301	DOPGSYSQMCETGYRLAADQHRCEDVDDCILBSPCORCVNTQGFECHCYPNYDLVDG	360
OY		360	ECVEPEVDPFCFRANCERYCOPLNQTSYLVCACAEFAPRI PHEPHNCOMFCNQTACPADCDPN	419
Dd		361	ECVEPEVDPFCFRANCERYCOPLNQTSYLVCACAEFAPRI PHEPHNCOMFCNQTACPADCDPN	420
OY		420	TOASECPREPGYILLDOGFICTDIDECENNGRCSGCVNLTPETFECTGGPSDALRHIGTDC	479
Dd		421	TOASECPREPGYILLDOGFICTDIDECENNGRCSGCVNLTPETFECTGGPSDALRHIGTDC	480
OY		480	DSGKYDGSGDSGSEPPSPPTPGSTTLRPRAVLVHGSLILGISIASISCLVVALALLACHLR	539
Dd		481	DSGKYDGSGDSGSEPPSPPTPGSTTLRPRAVLVHGSLILGISIASISCLVVALALLACHLR	540
OY		540	KKGGAARAMEYKCAAPSKEVVLQHVHTERTPORL	574
Dd		541	KKGGAARAMEYKCAAPSKEVVLQHVHTERTPORL	575
RESULT 2				
ID	ABM78950			
XX	ABM78950 standard; protein; 575 AA.			
AC	ABM78950;			
DT	15-JAN-2004 (first entry)			
DE	Breast cancer specific marker under-expressed in breast cancer.			
KW	Breast cancer; marker; thrombomodulin; human; diagnosis; cytostatic; biochip; vaccine.			

OS Homo sapiens.
XX
FN WO2003073911-A2.
XX
PD 12-SEP-2003.
XX
PE 27-FEB-2003; 2003WO-US005984.
XX
PR 28-FEB-2002; 2002US-0359999P.
XX
PA (GEOU) UNIV GEORGETOWN.
XX
PI Su YA, Yang J;
XX
DR WPT; 2003-721995/68.
XX
DR N-PESDB; ACF79930.
XX
XX
XX
XX
XX
PS Claim 5, Page 119-121; 143pp; English.

Claim 5; Page 119-121; 143pp; English.

The present sequence is that of a breast cancer specific marker (BCSM)

encoded by a gene identified by microarray gene expression analysis as being under-expressed in breast cancers in comparison to healthy tissue.

coagulation previously reported to be involved in vascular diseases and cancers. It is 1 of 19 (see ABM78941-59) BCSMs of the invention that are the BCSM was identified as LINCROMICUAIN (LINC), a negative regulator of

encoded by breast cancer specific genes (BCSGs) which are differentially expressed in breast cancer cell lines and breast cancer tissue samples as

compared to control cell lines and normal tissue samples. The invention provides a method for detection of breast cancer by measuring expression

transcribed from and polypeptides encoded by the BCSGs. A pharmaceutical formulation for the treatment of breast cancer comprises a BCSM, an

antibody directed against a BCSM, a vaccine generated using a BCSM, or an agent that modulates an expression level of a BCSG or an activity of a

BCSM. A biochip for diagnosing breast cancer or screening agents that inhibit breast cancer comprises a BCSG or BCSM

Sequence 575 AA;

every Match 99.2%; Score 3176.5; DB 7; Length 575;
 critical similarity 99.5%;
 critical similarity Pred No 6 1e-175.

[illegible]

1 MGLVLTGALALAGLGFPAPAEPPQGGSCQVEHDCFALYPGPATFNASQICDGLRGHLM 60

1 MLGVLVLTGALLAAGLGFPAPAEPPQGGSGCCEVHDCFPALYPGPATFPLNASQICDGLRGHEM 60

61 TVRSSVAADYISLLLENGDGGVSKRLMLGLQLPPSCGDPKRLGLFGRKFQVIVGDNINISIS 120

121 RWARLDINGAPLCGPICVASAAEATVPSEPIWEEOCEVKADGFLCEFHFPATCRPLAV 180

121 RWRDLNGAPLCGPLCAVSAEATVPSEPIWEEQCEVKADGFLCEHFHPATCRPLAV 180

181 EPGAAAAAVSTTYGTPFAARGADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHWAREAP 240

181 EFGAAAAVSITTYGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVQGHWAREAP 240

241 GAWDCSVENGCEHACNAIPGARPCQCPAGALOADGRSTAS-TQSCNDLCEHFCVNP 299

241 GAWDCSVENGCEHACNAIPGAPRCQCPAGALQADGRSCTASATOSCNDLCEHFCEVNP 300

300 DQPGSYSCWGETGYRLADQHRCEBDVDBCLBESBPCPRCRVNTGGFEHCYPNYDLVDG 359

300
301 DQPGSISLWCBIGIRLADQHCEDVDCLLEPSFCFQRCVNIQGGSECHCIFINIDVDS 300
360 ECVEVMBPCEBANCEYOCPINOTSYI,CVCAEGFAPIPHBPHRCMECNOTACPADCDPN 419

[illegible]

Db 361 ECEVPDPCFRANCEYQCQPLNQTSTYLCVCAEGFAPIPHEPRCOMFCNQTRACPADCDPN 420

Qy 420 TQASCEBEGYILDDGFICTDIDECENGFCGSGVCHNPGTFECICGPDALARRIGTDC 479

Db 421 TQASCEBEGYILDDGFICTDIDECENGFCGSGVCHNPGTFECICGPDALARRIGTDC 480

Qy 480 DSGKYDGDSDSGSGEPSPPTGSTLTTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539

Db 481 DSGKYDGDSDSGSGEPSPPTGSTLTTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540

Qy 540 KKQGAARAKMEYKCAAPSKEVVLQHVTRTERPQRL 574

Db 541 KKQGAARAKMEYKCAAPSKEVVLQHVTRTERPQRL 575

RESULT 3

AD54760

ID AD54760 standard; protein; 575 AA.

XX ADE54760;

AC

XX

DT 29-JAN-2004 (first entry)

XX

DE Human Protein P07204, SEQ ID NO 565.

XX

KM Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KM spared nerve injury; SNI; Chung.

XX

OS Homo sapiens.

XX

PN WO2003016475-A2.

XX

PD 27-FEB-2003.

XX

PF 14-AUG-2002; 2002WO-US025765.

XX

PR 14-AUG-2001; 2001US-0312147P.

XX

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX

PI Woolf C, D'urso D, Befort K, Costigan M;

PI WPI; 2003-268312/26.

DR GENBANK; P07204.

XX

PT New composition comprising two or more isolated polypeptides, useful for

XX preparing a medicament for treating pain in an animal.

XX

PS Claim 1; Page; 1017pp; English.

XX

CC The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating

CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that

CC modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene

CC therapy). The sequence presented is a human protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIP0 at

CC ftp.wipo.int/pub/published_pct_sequences.

XX

Qy Sequence 575 AA;

XX

Query Match 99.2%; Score 3176.5; DB 7; Length 575;

Best Local Similarity 99.5%; Fred. No. 6.1e-175;

Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 MLGVLVGLALALAGFPAPAPAPQPGSGQCYEHQCFALYPAPATFLNLSQICDGLRHLM 60

Db 1 MLGVLVGLALALAGFPAPAPAPQPGSGQCYEHQCFALYPAPATFLNLSQICDGLRHLM 60

Qy 61 TVRSSVAADVLSLLNGDGVGRRRLWIGQLPPGCGDPKRLGPRFQWVTGDNNTSYS 120

Db 61 TVRSSVAADVLSLLNGDGVGRRRLWIGQLPPGCGDPKRLGPRFQWVTGDNNTSYS 120

Qy 121 RWARLDLNGAPLCPPLCYAVSAEAATVPSSEPIWEEQCEYKADGFLCEFHPPATCRPLAV 180

Db 121 RWARLDLNGAPLCPPLCYAVSAEAATVPSSEPIWEEQCEYKADGFLCEFHPPATCRPLAV 180

Qy 181 EPGAAAVAVSTITGPPFAARGADFOALPVGSSAAVAPLGLQLMCTAPAGAVQGHMARAP 240

Db 181 EPGAAAVAVSTITGPPFAARGADFOALPVGSSAAVAPLGLQLMCTAPAGAVQGHMARAP 240

Qy 241 GAMDCSVENGCEHAACNAIPGARPOCCPAGALQADGNSCTAS-TQSCNDLCEHFCVENP 299

Db 241 GAMDCSVENGCEHAACNAIPGARPOCCPAGALQADGNSCTASATQSCNDLCEHFCVENP 300

Qy 300 DQPGSYCMCTGTGRLAADQRCBVDVDCILEPSPFCPCRVNTQGFECFCYPNVDLVG 359

Db 301 DQPGSYCMCTGTGRLAADQRCBVDVDCILEPSPFCPCRVNTQGFECFCYPNVDLVG 360

Qy 360 ECEVPDPCFRANCEYQCQPLNQTSTYLCVCAEGFAPIPHEPRCOMFCNQTRACPADCDPN 419

Db 361 ECEVPDPCFRANCEYQCQPLNQTSTYLCVCAEGFAPIPHEPRCOMFCNQTRACPADCDPN 420

Qy 420 TQASCEBEGYILDDGFICTDIDECENGFCGSGVCHNPGTFECICGPDALARRIGTDC 479

Db 421 TQASCEBEGYILDDGFICTDIDECENGFCGSGVCHNPGTFECICGPDALARRIGTDC 480

Qy 480 DSGKYDGDSDSGSGEPSPPTGSTLTTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539

Db 481 DSGKYDGDSDSGSGEPSPPTGSTLTTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540

Qy 540 KKQGAARAKMEYKCAAPSKEVVLQHVTRTERPQRL 574

Db 541 KKQGAARAKMEYKCAAPSKEVVLQHVTRTERPQRL 575

RESULT 4

ADD48168

ID ADD48168 standard; protein; 575 AA.

XX

AC ADD48168;

XX

DT 02-DEC-2004 (revised)

XX

DT 29-JAN-2004 (first entry)

XX

DE Human Protein NP_000352, SEQ ID NO 1386C.

XX

KM Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KM spared nerve injury; SNI; Chung.

XX

OS Homo sapiens.

OS Undefined.

XX WO2003016475-A2.
 XX
 XX 27-FEB-2003.
 PD
 XX 14-AUG-2002; 2002WO-US025765.
 PF
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 XX Woolf C, D'urso D, Befort K, Costigan M;
 PI
 XX WPI: 2003-268312/26.
 DR GENBANK; NP_000352.
 DR
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 XX Example 1; Page; 1017pp; English.
 PS
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNi), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (described in Table 3
 CC of the specification) which is differentially expressed during pain.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 575 AA;
 SQ
 Query Match 99.2%; Score 3176.5; DB 7; Length 575;
 Best Local Similarity 99.5%; Pred. No. 6.1e-175;
 Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 241 GAMDCEVNGGCEHAICNAIPGAPCCCPAGAAIADGSECTAS-TGSCNDICEHFCTVNP 299
 |||||
 DB 241 GAMDCEVNGGCEHAICNAIPGAPCCCPAGAAIADGSECTAS-TGSCNDICEHFCTVNP 300
 QY 300 DQGSYSQMCETGRIALADQRCEVDVDCILESPRCORCVNTQSGFCHCYPNYDLYDG 359
 |||||
 DB 301 DQGSYSQMCETGRIALADQRCEVDVDCILESPRCORCVNTQSGFCHCYPNYDLYDG 360
 QY 360 ECVEPVDPCEFRANCEYQOQPLNQTSTYLCVCAEGFAP1PHEBHRQMFQNCQTAACPADCPN 419
 |||||
 DB 361 ECVEPVDPCEFRANCEYQOQPLNQTSTYLCVCAEGFAP1PHEBHRQMFQNCQTAACPADCPN 420
 QY 420 TQASCECEBGYILDGFICTDIDECENGFGSCVGNLPGTFECICGPDALAHIGTDC 479
 |||||
 DB 421 TQASCECEBGYILDGFICTDIDECENGFGSCVGNLPGTFECICGPDALAHIGTDC 480
 QY 480 DSGKVDGSDSGSPSPPTGSLTPPAVGLVHSGLLIGISIASLCIVALLALCHLR 539
 |||||
 DB 481 DSGKVDGSDSGSPSPPTGSLTPPAVGLVHSGLLIGISIASLCIVALLALCHLR 540
 QY 540 KKGGAARAKMEYKCAAPSKEVVLQHVTERTPQRL 574
 |||||
 DB 541 KKGGAARAKMEYKCAAPSKEVVLQHVTERTPQRL 575
 |||||
 RESULT 5
 ADN04006
 ID ADN04006 standard; protein, 575 AA.
 AC ADN04006;
 XX 01-JUL-2004 (first entry)
 DT
 XX
 DE Antipsoriatic protein sequence #198.
 KM antipsoriatic; gene therapy; psoriasis; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2004028479-A2.
 XX
 PD 08-APR-2004.
 XX
 PF 25-SEP-2003; 2003WO-US030907.
 XX
 PR 25-SEP-2002; 2002US-0414006P.
 XX
 PA (GENTECH) GENENTECH INC.
 XX
 PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
 PI Wu TD;
 PI
 DR WPI: 2004-305105/28.
 DR N-PSDB; ADN04005.
 PT New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.
 PS Claim 9; SEQ ID NO 400; 3669pp; English.
 XX
 CC The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.
 XX
 SQ Sequence 575 AA;
 Query Match 99.2%; Score 3176.5; DB 8; Length 575;
 Best Local Similarity 99.5%; Pred. No. 6.1e-175;
 Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MLGVLVIGALALAGLGPAPAPAPPGSSQCYEHDCFLALYPGPATFLNASQICDGLRGLTM 60
 Db 1 MLGVLVIGALALAGLGPAPAPAPPGSSQCYEHDCFLALYPGPATFLNASQICDGLRGLTM 60
 QY 61 TVRSSVADVLSLLNBDGGVGRRLMTGLQPPGCGDKRLGRLRGFWTGDNNNTSYS 120
 Db 61 TVRSSVADVLSLLNBDGGVGRRLMTGLQPPGCGDKRLGRLRGFWTGDNNNTSYS 120
 QY 121 RMARLDLNGAPLCPGLCYAVSAEAATVSEPIWEEQCEVADGFLCEFHFPATCRPLAV 180
 Db 121 RMARLDLNGAPLCPGLCYAVSAEAATVSEPIWEEQCEVADGFLCEFHFPATCRPLAV 180
 QY 181 EPGAAAASVITTYGTPPARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVQGHAREAP 240
 Db 181 EPGAAAASVITTYGTPPARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVQGHAREAP 240
 QY 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSSCTASATQSCNDLCEHFVNP 299
 Db 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSSCTASATQSCNDLCEHFVNP 300
 QY 300 DPGSSYSCMCTGYRLAADQHRCEVDVDCILEPSPCPCPCVNTQGFECCHYPNYDLVDG 359
 Db 301 DPGSSYSCMCTGYRLAADQHRCEVDVDCILEPSPCPCPCVNTQGFECCHYPNYDLVDG 360
 QY 360 ECVEVPDPCFRANCEYCOQPLNQTSYLVCAGFAPIPHEPHRCQMFNCQTAACPADCDPN 419
 Db 361 ECVEVPDPCFRANCEYCOQPLNQTSYLVCAGFAPIPHEPHRCQMFNCQTAACPADCDPN 420
 QY 420 TQASCECEBGYILDDGFICTDIDECENGFCGVCCHNLPGTFECTICGPDALARIHIGTDC 479
 Db 421 TQASCECEBGYILDDGFICTDIDECENGFCGVCCHNLPGTFECTICGPDALARIHIGTDC 480
 QY 480 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALCLHR 539
 Db 481 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALCLHR 540
 QY 540 KKQGAARAKMEYKCAAPSKKEVVLQHVTERTPORL 574
 Db 541 KKQGAARAKMEYKCAAPSKKEVVLQHVTERTPORL 575

RESULT 6
 ADP12616
 ID ADP12616 standard; protein; 575 AA.
 AC ADP12616;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Protein encoded by mRNA of the invention #226.
 XX
 KW transplant rejection; immune system; rheumatoid arthritis; lupus;
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
 XX
 OS Homo sapiens.
 PN WO2004042346-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 24-APR-2003; 2003WO-US012946.
 XX
 PR 24-APR-2002; 2002US-00131831.
 XX
 PR 20-DEC-2002; 2002US-00325899.
 XX
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 XX
 PI Mohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 PI Rosenberg S;
 XX
 DR WPI; 2004-400724/37.
 XX

PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 PT rejection, in an individual, comprises detecting the expression level of
 PT the genes.
 XX
 PS Claim 65; SEQ ID NO 2625; 1762bp; English.
 XX
 CC The present invention relates to diagnosing or monitoring transplant
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 CC comprises detecting the expression level of one or more genes. The
 CC methods, system and kits are useful in diagnosing or monitoring
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 CC islet, lung, bone marrow or stem cell transplant rejection, in an
 CC xenotransplant rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC an individual. The methods are also useful in diagnosing and monitoring
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents a
 CC protein that is encoded by the mRNA of the invention.
 CC
 SQ Sequence 575 AA;
 Query Match 99.2%; Score 3176.5; DB 8; Length 575;
 Best Local Similarity 99.5%; Pred. No. 6.1e-175;
 Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 1 MLGVLVIGALALAGLGPAPAPAPPGSSQCYEHDCFLALYPGPATFLNASQICDGLRGLTM 60
 Db 1 MLGVLVIGALALAGLGPAPAPAPPGSSQCYEHDCFLALYPGPATFLNASQICDGLRGLTM 60
 QY 61 TVRSSVADVLSLLNBDGGVGRRLMTGLQPPGCGDKRLGRLRGFWTGDNNNTSYS 120
 Db 61 TVRSSVADVLSLLNBDGGVGRRLMTGLQPPGCGDKRLGRLRGFWTGDNNNTSYS 120
 QY 121 RMARLDLNGAPLCPGLCYAVSAEAATVSEPIWEEQCEVADGFLCEFHFPATCRPLAV 180
 Db 121 RMARLDLNGAPLCPGLCYAVSAEAATVSEPIWEEQCEVADGFLCEFHFPATCRPLAV 180
 QY 181 EPGAAAASVITTYGTPPARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVQGHAREAP 240
 Db 181 EPGAAAASVITTYGTPPARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVQGHAREAP 240
 QY 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSSCTASATQSCNDLCEHFVNP 299
 Db 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSSCTASATQSCNDLCEHFVNP 300
 QY 300 DPGSSYSCMCTGYRLAADQHRCEVDVDCILEPSPCPCPCVNTQGFECCHYPNYDLVDG 359
 Db 301 DPGSSYSCMCTGYRLAADQHRCEVDVDCILEPSPCPCPCVNTQGFECCHYPNYDLVDG 360
 QY 360 ECVEVPDPCFRANCEYCOQPLNQTSYLVCAGFAPIPHEPHRCQMFNCQTAACPADCDPN 419
 Db 361 ECVEVPDPCFRANCEYCOQPLNQTSYLVCAGFAPIPHEPHRCQMFNCQTAACPADCDPN 420
 QY 420 TQASCECEBGYILDDGFICTDIDECENGFCGVCCHNLPGTFECTICGPDALARIHIGTDC 479
 Db 421 TQASCECEBGYILDDGFICTDIDECENGFCGVCCHNLPGTFECTICGPDALARIHIGTDC 480
 QY 480 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALCLHR 539
 Db 481 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALCLHR 540
 QY 540 KKQGAARAKMEYKCAAPSKKEVVLQHVTERTPORL 574
 Db 541 KKQGAARAKMEYKCAAPSKKEVVLQHVTERTPORL 575

RESULT 7
 ADO28681
 ID ADO28681 standard; protein; 575 AA.
 AC ADO28681;
 XX

XX 12-AUG-2004 (first entry)
DT Human thrombomodulin protein SEQ ID NO:110.
XX
XX
DE high-grade dysplasia; HGD; oesophageal adenocarcinoma;
KM neo-plastic transformation; cancer; cytostatic; gene therapy; human;
KM thrombomodulin; chromosome 20.
XX
OS Homo sapiens.
XX
XX WO2004044178-A2.
XX
XX 27-MAY-2004.
XX
XX 13-NOV-2003; 2003WO-US036260.
XX
XX 13-NOV-2002; 2002US-0425813P.
XX
XX (GETH) GENENTECH INC.
XX
XX Smith V;
XX
XX WPI; 2004-420319/39.
XX
XX N-PSDB; ADO28680.
XX
XX Detecting of high-grade dysplasia in cells of a mammalian tissue sample
PT comprises establishing the level of expression in the test tissue sample
PT of the genes.
XX
XX Example 4; SEQ ID NO 110; 256pp; English.
XX
XX The present invention describes a method for detecting high-grade
XX dysplasia (HGD) in cells of a mammalian tissue sample. Also described:
XX (1) identifying an oesophageal tissue susceptible to oesophageal
XX adenocarcinoma; (2) determining the predispotion of a mammalian tissue
XX to a neo-plastic transformation by detecting HGD in cells of the tissue;
XX and (3) detecting cancer in a patient. The method can be used in
XX detecting HGD and cancer in cells of a mammalian tissue sample. The
XX method and compositions of the present invention can be used in treating
XX and preventing HGD and cancer, and in gene therapy. The present sequence
XX represents human thrombomodulin, which is used in the exemplification of
XX the present invention. The human thrombomodulin gene is located on
XX chromosome 20.
XX
XX Sequence 575 AA;
SQ
Query Match 99.2%; Score 3176.5; DB 8; Length 575;
Best Local Similarity 99.5%; Pred. No. 6; 1e-175;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 MLGVIVGALALAGGFPAPAPAPPGSGSCVHDFALYPPGATPLNLSQICDGRGHM 60
DB 1 MLGVIVGALALAGGFPAPAPAPPGSGSCVHDFALYPPGATPLNLSQICDGRGHM 60
QY 61 TYRSSVADVISILANGDGVGRRLMIGLQLPCCGDPKRLGPGQWVTGDNNTSYS 120
DB 61 TYRSSVADVISILANGDGVGRRLMIGLQLPCCGDPKRLGPGQWVTGDNNTSYS 120
QY 121 RWARLDINGAPICGFLCVAVSAEAATVSEPIWEEQCEVKADGFLCEFHFPATCRPLAV 180
DB 121 RWARLDINGAPICGFLCVAVSAEAATVSEPIWEEQCEVKADGFLCEFHFPATCRPLAV 180
QY 181 EPGAAGAAAVSTYTGPPAPARGADPQALPVGSSAAVAAPLGLQIMCTAPPAVGVGHAREAP 240
DB 181 EPGAAGAAAVSTYTGPPAPARGADPQALPVGSSAAVAAPLGLQIMCTAPPAVGVGHAREAP 240
QY 241 GAMDSVNGGCEHACNAIPGARPCQCPAGALQADGSECTAS-TQSCNDLCEHCVNP 299
DB 241 GAMDSVNGGCEHACNAIPGARPCQCPAGALQADGSECTASATQSCNDLCEHCVNP 300
QY 300 DQPGSYSCMCECTGYRLAADQHRCEVDDCILBSPSCQRCNTNOGCFECHCYPNYDLVDG 359
DB 300 DQPGSYSCMCECTGYRLAADQHRCEVDDCILBSPSCQRCNTNOGCFECHCYPNYDLVDG 359

DB 301 DQPGSYSCMCECTGYRLAADQHRCEVDDCILBSPSCQRCNTNOGCFECHCYPNYDLVDG 360
QY 360 ECVPEVPDPCFRANCEYQCCQPLNQTSYLVCACGAPAPIPHEPHRCOMFCNQTACPADCPN 419
DB 361 ECVPEVPDPCFRANCEYQCCQPLNQTSYLVCACGAPAPIPHEPHRCOMFCNQTACPADCPN 420
QY 420 TQASCECEPEGIILDDGFTCTDIDCEGNGFCSSGVCNHLPGFTEICGPBDSLAHHIGDC 479
DB 421 TQASCECEPEGIILDDGFTCTDIDCEGNGFCSSGVCNHLPGFTEICGPBDSLAHHIGDC 480
QY 480 DSGKYDGDSDSGSPSPPTGSLTTPPAVGLVHSGLLIGISIASLCLVALLALLGLTR 539
DB 481 DSGKYDGDSDSGSPSPPTGSLTTPPAVGLVHSGLLIGISIASLCLVALLALLGLTR 540
QY 540 KKQGAARAKMEYKCAAPSKEVVLQHVTERTPQRL 574
DB 541 KKQGAARAKMEYKCAAPSKEVVLQHVTERTPQRL 575
RESULT 8
ADP79506
ID ADP79506 standard; protein; 575 AA.
XX
XX ADP79506;
XX
XX 04-NOV-2004 (first entry)
XX
XX Human thrombomodulin.
DE Human thrombomodulin; gene therapy; vasotrophic; cardiovascular-gen.;
KM Human; thrombomodulin; gene therapy; vasotrophic; cardiovascular-gen.;
KM neotropic.
XX
XX Homo sapiens.
XX
XX WO2004050844-A2.
XX
XX 17-JUN-2004.
XX
XX 02-DEC-2003; 2003WO-US038125.
XX
XX 02-DEC-2002; 2002US-0430099P.
XX
XX (BIOV-) BIOVEC LLC.
XX
XX SenGall LR, Wong J;
PI
XX
XX WPI; 2004-461114/43.
XX
XX N-PSDB; ADP79507, ADP79508, ADP79510.
XX
XX Treating vascular diseases, e.g. atherosclerotic cardiovascular disease
PT comprises introducing a DNA sequence encoding a thrombomodulin protein or
PT its variant into a segment of a blood vessel using a gutless adenovirus
PT vector.
XX
XX Claim 2; SEQ ID NO 2; 44pp; English.
XX
XX The present sequence is that of human thrombomodulin (TM). The invention
XX relates to the ex vivo and in vivo expression of the TM gene for
XX treatment of vascular diseases. A method for treating a vascular disease
XX in a mammal comprises: infecting a segment of a blood vessel in vitro
XX using a gutless adenoviral vector which comprises a polynucleotide
XX encoding a thrombomodulin (TM) protein ADP79506 or its variant; and
XX grafting the virus-treated blood vessel in the mammal such that the TM
XX protein or its variant is expressed in an amount sufficient to reduce re-
XX occlusion or intimal hyperplasia in the grafted blood vessel. A method
XX for treating a vascular disease involves: evacuating a clot in a blood
XX vessel; isolating a segment of blood vessel around the evacuation site
XX with a balloon catheter; and infecting the segment of blood vessel in
XX vivo using a gutless adenoviral vector comprising a polynucleotide
XX encoding a TM protein or its variant, such that TM or its variant is
XX expressed in an amount sufficient to reduce re-occlusion or intimal
XX hyperplasia in the infected segment of the blood vessel. A further method
XX for treating a vascular disease comprises administering a gutless

Db 481 DSGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLLCHLR 540
 QY 540 KKGGAARAKMEYKCAAPSKEVVLQHVTERTPORL 574
 Db 541 KKGGAARAKMEYKCAAPSKEVVLQHVTERTPORL 575

RESULT 10

ADU06321 standard; protein, 575 AA.

ADU06321;

27-JAN-2005 (first entry)

Novel bronchial cancer-associated human protein SeqID545.

bronchial cancer; cytostatic; tumour-associated protein;

cancer detection; metastasis; tumour; human.

Homo sapiens.

DE10316701-A1.

04-NOV-2004.

09-APR-2003; 2003DE-01016701.

09-APR-2003; 2003DE-01016701.

(HINZ/) HINZMANN B.

(HERM/) HERMANN K.

(CAST/) HEIDEN CASTANOS-VELEZ E.

Mennerich D, Bruemendorf T, Heiden E, Hermann K, Kimmann H;

Li X, Roepcke S, Staub E, Hinzmann B, Rosenthal A, Pilarsky C;

WPI; 2004-786403/78.

N-P5DB; ADU05634.

Claim 2; SEQ ID NO 545; 1381bp; German.

This invention relates to a novel isolated nucleic acid associated with

bronchial cancer comprising 489 defined sequences given in the

specification. The invention may be useful for the production of

compounds with a cytostatic activity through the inhibition of expression

or activity of tumour-associated proteins. The novel DNA sequences and

the proteins/peptides encoded by them are used for detecting bronchial

cancer or determining the risk of developing it and to screen for

specific binding partners of the DNA or protein sequences, where the

binding partners are potentially useful as agents for treating or

diagnosing bronchial cancer. The DNA or protein sequences can also be

used for prognosis, detection of metastases and for secondary treatment

(of tumours that have been stabilised or are no longer detectable).

Detecting abnormal expression of the DNA sequences provides early

diagnosis of bronchial cancers. The present sequence is that of a protein

encoded by a novel bronchial cancer-associated human gene sequence of the

invention.

Sequence 575 AA;

Query Match 99.2%; Score 3176.5; DB 8; Length 575;

Best Local Similarity 99.5%; Pred. No. 6.1e-175;

Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

1 MGVGVVGLAALAGAGFPAAPAPPOGSGSCVHDCFPALYPGPATPLNLSQICDGRGHL 60

1 MGVGVVGLAALAGAGFPAAPAPPOGSGSCVHDCFPALYPGPATPLNLSQICDGRGHL 60

1 MGVGVVGLAALAGAGFPAAPAPPOGSGSCVHDCFPALYPGPATPLNLSQICDGRGHL 60

QY 61 TVRSSVAADVITSLANGDGYGRRRLWIGLQIPGCCDPKRLGRLRGFQWYTGNNNTSYS 120
 Db 61 TVRSSVAADVITSLANGDGYGRRRLWIGLQIPGCCDPKRLGRLRGFQWYTGNNNTSYS 120
 QY 121 RMARLDLNGAPLCPPLCAVAASAATVPSBPIMEEOCEVADGFLCEFFHPATCRPLAV 180
 Db 121 RMARLDLNGAPLCPPLCAVAASAATVPSBPIMEEOCEVADGFLCEFFHPATCRPLAV 180
 QY 181 EPGAAAAAVSITYGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHAREAP 240
 Db 181 EPGAAAAAVSITYGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHAREAP 240
 QY 241 GAMDCSVENGCCEHACNAIPAPRCQCPAGALQADGSCFASATQSCNDICEHFCVNP 299
 Db 241 GAMDCSVENGCCEHACNAIPAPRCQCPAGALQADGSCFASATQSCNDICEHFCVNP 299
 QY 300 DQPSYSQMCETGRLAADHRCEDVDDCIIEPSPCPCPCVNTQGGFECPCPVNVDLVG 359
 Db 300 DQPSYSQMCETGRLAADHRCEDVDDCIIEPSPCPCPCVNTQGGFECPCPVNVDLVG 359
 QY 360 ECVEPVPDPCFRANCEYQCPINQTSYLCVCAEGFAP1PHEBRCQMFQACPADCDPN 419
 Db 360 ECVEPVPDPCFRANCEYQCPINQTSYLCVCAEGFAP1PHEBRCQMFQACPADCDPN 419
 QY 420 TVASCEPBEYITLDGFTCTIDECENGFCSCGCHNLPGTFECICGPDLSLAHIGTDC 479
 Db 420 TVASCEPBEYITLDGFTCTIDECENGFCSCGCHNLPGTFECICGPDLSLAHIGTDC 479
 QY 480 DSGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLLCHLR 539
 Db 480 DSGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLLCHLR 539
 QY 540 KKGGAARAKMEYKCAAPSKEVVLQHVTERTPORL 574
 Db 540 KKGGAARAKMEYKCAAPSKEVVLQHVTERTPORL 574
 QY 541 KKGGAARAKMEYKCAAPSKEVVLQHVTERTPORL 575
 Db 541 KKGGAARAKMEYKCAAPSKEVVLQHVTERTPORL 575

RESULT 11

ABG72572

ID ABG72572 standard; protein, 631 AA.

ABG72572;

05-MAR-2003 (first entry)

Human thrombomodulin protein #1 (CD141).

Human; thrombomodulin; CD141; dendritic cell separation; inflammation;

antiinflammatory; cytostatic; antiarthritic; antineumatic;

immunopressive; dermatological; cell therapy; dermatomyositis; cancer;

autoimmune disorder; rheumatoid arthritis; psoriatic arthritis;

alkylosing spondylitis; Sjorgen's syndrome; lupus erythematosus;

Goodpasture's syndrome; scleroderma; vasculitis; polyomyositis.

Homo sapiens.

WO200293172-A1.

21-NOV-2002.

17-MAY-2002; 2002WO-US015786.

17-MAY-2001; 2001US-0291561P.

(MILT-) MILTENYI BIOTEC INC.

Schmitz J, Dzlonk A, Buck DW;

WPI; 2003-129324/12.

Enriching for dendritic cells from a mixture of cells, useful for

treating inflammation, cancer or autoimmune disorders such as arthritis,

or lupus by contacting the mixture of cell with an antigen-binding

protein.

Enriching for dendritic cells from a mixture of cells, useful for

treating inflammation, cancer or autoimmune disorders such as arthritis,

or lupus by contacting the mixture of cell with an antigen-binding

protein.

Enriching for dendritic cells from a mixture of cells, useful for

treating inflammation, cancer or autoimmune disorders such as arthritis,

or lupus by contacting the mixture of cell with an antigen-binding

protein.

Enriching for dendritic cells from a mixture of cells, useful for

treating inflammation, cancer or autoimmune disorders such as arthritis,

or lupus by contacting the mixture of cell with an antigen-binding

protein.

PT fragment specific for CD141.

XX Example 1; Fig 3A; 88pp; English.

CC This invention relates to a novel method for separating dendritic cells
CC from a mixture of cells. The method comprises contacting the mixture of
CC cells with an antigen-binding fragment specific for CD141, and selecting
CC the cells that are CD141 positive therefore producing a dendritic cell-
CC enriched composition. The method of the invention may have
CC antiinflammatory, cytostatic, antiarthritic, antineumatic,
CC immunosuppressive and dermatological activities and may be used in cell
CC therapy. The methods, compositions and agents of the invention are useful
CC for treating inflammation, cancer or autoimmune disorders such as
CC rheumatoid arthritis, psoriatic arthritis, alkylosing spondylitis,
CC Sjogren's syndrome, lupus erythematosus, Goodpasture's syndrome,
CC scleroderma, vasculitis, polymyositis or dermatomyositis. The dendritic
CC cells and populations are useful for screening assays for agents that
CC affect dendritic cell function, and for the phenotypic, functional,
CC biochemical or molecular analyses of dendritic cells. The compositions
CC and dendritic cells are useful as vaccine adjuvants. The present sequence
CC represents a protein sequence of human CD141 protein which is used to
CC generate the dendritic cell specific antibodies that are used in the
CC method of the invention

XX Sequence 631 AA;

Query Match 99.2%; Score 3176.5; DB 6; Length 631;
Best Local Similarity 99.5%; Pred. No. 6.7e-175;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MLGVLVIGALALAGLGFPPAPAPBPQGSQCVHEHDCFALYPGPATFLNASQICDGLRGHLM 60
DB 57 MLGVLVIGALALAGLGFPPAPAPBPQGSQCVHEHDCFALYPGPATFLNASQICDGLRGHLM 116
QY 61 TVRSSVADAVISLLINGDGGVGRRLMTGLQIPGCGDPKRLGPRGFQWMTGDNNTSYS 120
DB 117 TVRSSVADAVISLLINGDGGVGRRLMTGLQIPGCGDPKRLGPRGFQWMTGDNNTSYS 176
QY 121 RMAFLDLNGALPCGPLCYAASAABATVPSPIWEQCEVADGFLCFHPATCRPLAV 180
DB 177 RMAFLDLNGALPCGPLCYAASAABATVPSPIWEQCEVADGFLCFHPATCRPLAV 236
QY 181 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVQGHAREAP 240
DB 237 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVQGHAREAP 296
QY 241 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSSCTAS-TQSCNDLCCEHFCVNP 299
DB 297 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSSCTASATQSCNDLCCEHFCVNP 356
QY 300 DQPSYSQMCCTGYRLADQRCEDVDCTILEPSPQRCVNTQSGFECCHCPYNDLVDS 359
DB 357 DQPSYSQMCCTGYRLADQRCEDVDCTILEPSPQRCVNTQSGFECCHCPYNDLVDS 416
QY 360 ECVBPVDPCEFRANCEYQCPINQTSYLCVCAEGFAPLIPHEBHRQMFQNCQTACPADCDPN 419
DB 417 ECVBPVDPCEFRANCEYQCPINQTSYLCVCAEGFAPLIPHEBHRQMFQNCQTACPADCDPN 476
QY 420 TQASCECEBYITLDGFICTDIDCEGNGFCGSCVCHNLPGTFECTCGPSALARRHTGDC 479
DB 477 TQASCECEBYITLDGFICTDIDCEGNGFCGSCVCHNLPGTFECTCGPSALARRHTGDC 536
QY 480 DSGVNDGSDSGSPBPPTPGSTLTTPAVGLVHSGLLIGISIASLCLVALLALCLHR 539
DB 537 DSGVNDGSDSGSPBPPTPGSTLTTPAVGLVHSGLLIGISIASLCLVALLALCLHR 596
QY 540 KKQGAARAKMEYKCAAPSEKVVLAQHRTERTFORL 574
DB 597 KKQGAARAKMEYKCAAPSEKVVLAQHRTERTFORL 631

RESULT 12
ADN05602

ID ADN05602 standard; protein; 681 AA.

XX AC ADN05602;

XX DT 01-JUL-2004 (first entry)

XX DE Antipsoriatic protein sequence #966.

XX KW antipsoriatic; gene therapy; psoriasis; diagnosis.

OS Homo sapiens.

XX PN WO2004028479-A2.

XX PD 08-APR-2004.

XX PF 25-SEP-2003; 2003WO-US030907.

XX PR 25-SEP-2002; 2002US-0414006P.

XX PA (GETH) GENENTECH INC.

PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;

XX DR WPI; 2004-305105/28.

XX DR N-PSDB; ADN05601.

PT New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.

PS Claim 9; SEQ ID NO 1996; 3069pp; English.

CC The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.

XX SQ Sequence 681 AA;

Query Match 99.2%; Score 3176.5; DB 8; Length 681;
Best Local Similarity 99.5%; Pred. No. 7.2e-175;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MLGVLVIGALALAGLGFPPAPAPBPQGSQCVHEHDCFALYPGPATFLNASQICDGLRGHLM 60
DB 107 MLGVLVIGALALAGLGFPPAPAPBPQGSQCVHEHDCFALYPGPATFLNASQICDGLRGHLM 166
QY 61 TVRSSVADAVISLLINGDGGVGRRLMTGLQIPGCGDPKRLGPRGFQWMTGDNNTSYS 120
DB 167 TVRSSVADAVISLLINGDGGVGRRLMTGLQIPGCGDPKRLGPRGFQWMTGDNNTSYS 226
QY 121 RMAFLDLNGALPCGPLCYAASAABATVPSPIWEQCEVADGFLCFHPATCRPLAV 180
DB 227 RMAFLDLNGALPCGPLCYAASAABATVPSPIWEQCEVADGFLCFHPATCRPLAV 286
QY 181 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVQGHAREAP 240
DB 287 EPGAAAASVITTYGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVQGHAREAP 346
QY 241 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSSCTAS-TQSCNDLCCEHFCVNP 299
DB 347 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSSCTASATQSCNDLCCEHFCVNP 406
QY 300 DQPSYSQMCCTGYRLADQRCEDVDCTILEPSPQRCVNTQSGFECCHCPYNDLVDS 359
DB 407 DQPSYSQMCCTGYRLADQRCEDVDCTILEPSPQRCVNTQSGFECCHCPYNDLVDS 466
QY 467 ECVBPVDPCEFRANCEYQCPINQTSYLCVCAEGFAPLIPHEBHRQMFQNCQTACPADCDPN 526

QY 420 TQASCECEBEYIILDDGFICTDIDECENGFCSCGVCHNLPGTFECICGPDSSALAHIGTDC 479
DB 527 TQASCECEBEYIILDDGFICTDIDECENGFCSCGVCHNLPGTFECICGPDSSALAHIGTDC 586
QY 480 DSGKVDGSDSGSGPPSPPTGSLTPPAVGLVHSGLLIGISISLCLVALLLCHLR 539
DB 587 DSGKVDGSDSGSGPPSPPTGSLTPPAVGLVHSGLLIGISISLCLVALLLCHLR 646
QY 540 KKQGAARAKMEYKCAAPSKEVVLQHVTERTPORL 574
DB 647 KKQGAARAKMEYKCAAPSKEVVLQHVTERTPORL 681

RESULT 13
AAR1534
ID AAR1534 standard; protein; 575 AA.
AC AAR1534;
XX 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 17-JUN-1991 (first entry)
XX Human thrombomodulin type II polypeptide.
DE Thrombomodulin; chondroitin; protein C; thrombin; thrombolytic;
KW chondroitin sulphate; anticoagulant; myocardial infarction.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..18
FT /label= signal peptide
FT 19..365
FT /label= opt. N-terminal sequence
FT Peptide 366..480
FT /label= human thrombomodulin active fragment
FT Peptide 481..516
FT /label= opt. C-terminal sequence

W09104276-A.
PD 04-APR-1991.
XX 25-SEP-1989; 89JP-00246270.
PF 25-SEP-1989; 89JP-00246270.
PR 25-SEP-1989; 89JP-00246270.
XX (ASAH) ASAH KASEI KOGYO KK.
XX Yamamoto S, Gomi K, Ogawa K;
PI WPI; 1991-117478/16.
XX New human thrombomodulin polypeptide contg. chondroitin - has
PT anticoagulant platelet agglutination and thrombolytic activity.
XX
PS Disclosure; Fig 1; 80pp; Japanese.
XX This human thrombomodulin polypeptide comprises a 115 residue active
CC fragment with opt. flanking sequences (N-terminal= 347 amino acids; C-
CC terminal= 36 amino acids). Additionally it has an N-terminal signal
CC sequence and an attached sugar chain, contg. chondroitin or chondroitin
CC sulphate. It promotes the activation of protein C by thrombin and has
CC good anticoagulant, platelet aggregation inhibition and thrombolytic
CC activities. It can therefore be used for treating cardiovascular
CC diseases, eg arteriosclerosis or myocardial infarction. (Updated on 09-
CC JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
XX Sequence 575 AA;
SQ

Query Match 99.0%; Score 3172.5; DB 2; Length 575;
Beet Local Similarity 99.3%; Pred. No. 1e-174;
Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 MLGVLVGLALALAGFPAPPAEPPOGSGQCEVHDCFPALYGPATFTLNASQICDLRGHLM 60
DB 1 MLGVLVGLALALAGFPAPPAEPPOGSGQCEVHDCFPALYGPATFTLNASQICDLRGHLM 60
QY 61 TVRSSVADYVLSLLNDGGVGRRLMWIGQLPPGCCDPKRLGRLGPOVYTGNNNTSYS 120
DB 61 TVRSSVADYVLSLLNDGGVGRRLMWIGQLPPGCCDPKRLGRLGPOVYTGNNNTSYS 120
QY 121 RMARLDNGAPLCPPLCVAAVSAATYPSPIWEEOCEVYKADDFLCEFHPPACRPLAV 180
DB 121 RMARLDNGAPLCPPLCVAAVSAATYPSPIWEEOCEVYKADDFLCEFHPPACRPLAV 180
QY 181 ERGAAAANVSTYGTTPPAARGADFOALPVGSSAAVAFLGLQMLCTAPGAVQGMAREAP 240
DB 181 ERGAAAANVSTYGTTPPAARGADFOALPVGSSAAVAFLGLQMLCTAPGAVQGMAREAP 240
QY 241 GAMDCSVENGGCEHACNAIPGARPQC PAGALQADGRSCTAS-TQSCNDICEHFVYPNP 299
DB 241 GAMDCSVENGGCEHACNAIPGARPQC PAGALQADGRSCTAS-TQSCNDICEHFVYPNP 300
QY 300 DQPSYSCMCTGYRLAADQRCEDVDCLIEBSPCQRCVNTGGFECHECYMYDLVDG 359
DB 301 DQPSYSCMCTGYRLAADQRCEDVDCLIEBSPCQRCVNTGGFECHECYMYDLVDG 360
QY 360 ECVFVPDPCFRANCEYOCPLANTSYLVCVCEGAPAPIPHEBRCQMCNQTACPADCDPN 419
DB 361 ECVFVPDPCFRANCEYOCPLANTSYLVCVCEGAPAPIPHEBRCQMCNQTACPADCDPN 420
QY 420 TQASCECEBEYIILDDGFICTDIDECENGFCSCGVCHNLPGTFECICGPDSSALAHIGTDC 479
DB 421 TQASCECEBEYIILDDGFICTDIDECENGFCSCGVCHNLPGTFECICGPDSSALAHIGTDC 480
QY 480 DSGKVDGSDSGSGPPSPPTGSLTPPAVGLVHSGLLIGISISLCLVALLLCHLR 539
DB 481 DSGKVDGSDSGSGPPSPPTGSLTPPAVGLVHSGLLIGISISLCLVALLLCHLR 540
QY 540 KKQGAARAKMEYKCAAPSKEVVLQHVTERTPORL 574
DB 541 KKQGAARAKMEYKCAAPSKEVVLQHVTERTPORL 575

RESULT 14
AAR41806
ID AAR41806 standard; peptide; 575 AA.
AC AAR41806;
XX 30-MAR-1994 (first entry)
DT Thrombomodulin.
DE Transformation; fungus; blood coagulation; prevention; platelet;
KW aggregation; thrombolytic activity; thrombolytic; human thrombomodulin;
KW site-directed mutagenesis; promotion; protein C; activation; thrombin.
OS Homo sapiens.
XX JP05213998-A.
XX 24-AUG-1993.
XX 02-AUG-1991; 91JP-00282369.
XX 03-AUG-1990; 90JP-00204978.
XX 30-JUL-1991; 91JP-00189984.
XX (ASAH) ASAHI CHEM IND CO LTD.
XX WPI; 1993-299652/38.
DR

XX Novel polypeptide obtd. by culturing transformed fungus - having blood
 PT coagulation preventing, platelet aggregation preventing and thrombolytic
 PT activities.
 XX
 XX Disclosure; Fig 55; 65pp; Japanese.
 XX
 CC Novel polypeptides, obtd. by culturing transformed fungus, have blood
 CC coagulation preventing, platelet aggregation preventing and thrombolytic
 CC activities. In an example, plasmid M3impl19TMJ3 (constructed from pSV2TMJ2
 CC (ATCC 67228) contg. a human thrombomodulin sequence) was subjected to
 CC site directed mutagenesis to prepare pSV2TMJ7. Plasmid pSV2TMJ7 was
 CC transfected to COS-1 cells. The activity of promoting protein C
 CC activation by thrombin of the peptide produced by the transformed COS-1
 CC cell was measured. The amt. of the peptide was determined
 CC
 XX Sequence 575 AA;
 SQ
 Query Match 99.0%; Score 3172.5; DB 2; Length 575;
 Best Local Similarity 99.3%; Pred. No. 1e-174;
 Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 MLGVLVIGALNLAGLGFPPAPAPPOGSGQCVHDCFALYPGATFLNASQICDGLRGHLM 60
 DB 1 MLGVLVIGALNLAGLGFPPAPAPPOGSGQCVHDCFALYPGATFLNASQICDGLRGHLM 60
 QY 61 TVRSSVADVLSILNLDGQVGRRLMTGLQLPFGCGDPKRLGRLGFGQWVTGDNNTSYS 120
 DB 61 TVRSSVADVLSILNLDGQVGRRLMTGLQLPFGCGDPKRLGRLGFGQWVTGDNNTSYS 120
 QY 121 RWARLDLNGAPLCPGLCVAVSAEAATVSEPIWEOQCEVADGFLCEHFHPATCRPLAV 180
 DB 121 RWARLDLNGAPLCPGLCVAVSAEAATVSEPIWEOQCEVADGFLCEHFHPATCRPLAV 180
 QY 121 RWARLDLNGAPLCPGLCVAVSAEAATVSEPIWEOQCEVADGFLCEHFHPATCRPLAV 180
 DB 121 RWARLDLNGAPLCPGLCVAVSAEAATVSEPIWEOQCEVADGFLCEHFHPATCRPLAV 180
 QY 181 EPGAAAASVSTTGGPPARAGADFOALPVGSSAAVAAPLGLQMLCTAPGAAVGHARBAR 240
 DB 181 EPGAAAASVSTTGGPPARAGADFOALPVGSSAAVAAPLGLQMLCTAPGAAVGHARBAR 240
 QY 181 EPGAAAASVSTTGGPPARAGADFOALPVGSSAAVAAPLGLQMLCTAPGAAVGHARBAR 240
 DB 181 EPGAAAASVSTTGGPPARAGADFOALPVGSSAAVAAPLGLQMLCTAPGAAVGHARBAR 240
 QY 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSRCTAS-TQSCNDLCEHFCEVNP 299
 DB 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSRCTAS-TQSCNDLCEHFCEVNP 299
 QY 300 DQPGSYSCMCTGYRLAADQHRCEVDVDCILPSPCPORCVNTQGFCHCYPNYDLVDG 359
 DB 300 DQPGSYSCMCTGYRLAADQHRCEVDVDCILPSPCPORCVNTQGFCHCYPNYDLVDG 359
 QY 301 DQPGSYSCMCTGYRLAADQHRCEVDVDCILPSPCPORCVNTQGFCHCYPNYDLVDG 360
 DB 301 DQPGSYSCMCTGYRLAADQHRCEVDVDCILPSPCPORCVNTQGFCHCYPNYDLVDG 360
 QY 360 ECVFVNDPCFRANCYOCQPLNQTSTYLCVCAEGFAPLPHBPRCOMFCNQTACPADCPN 419
 DB 360 ECVFVNDPCFRANCYOCQPLNQTSTYLCVCAEGFAPLPHBPRCOMFCNQTACPADCPN 419
 QY 361 ECVFVNDPCFRANCYOCQPLNQTSTYLCVCAEGFAPLPHBPRCOMFCNQTACPADCPN 420
 DB 361 ECVFVNDPCFRANCYOCQPLNQTSTYLCVCAEGFAPLPHBPRCOMFCNQTACPADCPN 420
 QY 420 TOASCECEGYILDDGFICTDIDECENGFGSGVCHNLPGTPECICGPDALARIHTGDC 479
 DB 420 TOASCECEGYILDDGFICTDIDECENGFGSGVCHNLPGTPECICGPDALARIHTGDC 479
 QY 421 TOASCECEGYILDDGFICTDIDECENGFGSGVCHNLPGTPECICGPDALARIHTGDC 480
 DB 421 TOASCECEGYILDDGFICTDIDECENGFGSGVCHNLPGTPECICGPDALARIHTGDC 480
 QY 480 DSGKVDGSDSGSBPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
 DB 480 DSGKVDGSDSGSBPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
 QY 481 DSGKVDGSDSGSBPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540
 DB 481 DSGKVDGSDSGSBPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540
 QY 540 KKQGAARAKMEYKCAAPSKVVLQHVTERTEPQRL 574
 DB 541 KKQGAARAKMEYKCAAPSKVVLQHVTERTEPQRL 575
 RESULT 15
 AAR43031
 ID AAR43031 standard; protein; 575 AA.
 AC AAR43031;
 XX
 XX 25-MAR-2003 (revised)
 DT 16-MAY-1994 (first entry)
 XX
 XX Human thrombomodulin.

XX Anticoagulant; platelet aggregation inhibitor; protein C; activation;
 KW thrombin; thrombomodulin; coagulation disorder; thrombosis;
 KW myocardial infarction; embolism; telangiectasia;
 KW arteriosclerosis obliterans; disseminated intravascular coagulation; DIC;
 KW angina pectoris; gestosis; transient ischaemic attack.
 XX
 XX Homo sapiens.
 XX
 XX WO9322447-A1.
 XX
 XX 11-NOV-1993.
 XX
 XX 30-APR-1993; 93WO-JP000578.
 XX
 XX 01-MAY-1992; 92JP-00112903.
 XX
 XX (ASAH) ASAH KASEI KOGYO KK.
 XX
 XX Zushi M, Kondo S, Toma K;
 XX
 XX WPI, 1993-368806/46.
 XX
 XX Peptide with anticoagulant and platelet aggregation inhibitor activity -
 PT which promotes protein C activation by thrombin and is useful in treating
 PT coagulation disorders e.g. thrombosis.
 XX
 XX Disclosure; Fig 1; 84pp; Japanese.
 XX
 CC New peptides (see AAR50069) are inhibitors of the blood coagulation and
 CC platelet aggregation activities of thrombin and promote the protein-C
 CC activation effect of thrombin. They can be produced efficiently in pure
 CC form by culture of appropriate transformants, and are useful in treatment
 CC of circulatory disorders such as myocardial infarction, thrombosis,
 CC embolism, telangiectasia, arteriosclerosis obliterans, disseminated
 CC intravascular coagulation, angina pectoris, gestosis and transient
 CC ischaemic attack. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX Sequence 575 AA;
 SQ
 Query Match 99.0%; Score 3172.5; DB 2; Length 575;
 Best Local Similarity 99.3%; Pred. No. 1e-174;
 Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 MLGVLVIGALNLAGLGFPPAPAPPOGSGQCVHDCFALYPGATFLNASQICDGLRGHLM 60
 DB 1 MLGVLVIGALNLAGLGFPPAPAPPOGSGQCVHDCFALYPGATFLNASQICDGLRGHLM 60
 QY 61 TVRSSVADVLSILNLDGQVGRRLMTGLQLPFGCGDPKRLGRLGFGQWVTGDNNTSYS 120
 DB 61 TVRSSVADVLSILNLDGQVGRRLMTGLQLPFGCGDPKRLGRLGFGQWVTGDNNTSYS 120
 QY 121 RWARLDLNGAPLCPGLCVAVSAEAATVSEPIWEOQCEVADGFLCEHFHPATCRPLAV 180
 DB 121 RWARLDLNGAPLCPGLCVAVSAEAATVSEPIWEOQCEVADGFLCEHFHPATCRPLAV 180
 QY 121 RWARLDLNGAPLCPGLCVAVSAEAATVSEPIWEOQCEVADGFLCEHFHPATCRPLAV 180
 DB 121 RWARLDLNGAPLCPGLCVAVSAEAATVSEPIWEOQCEVADGFLCEHFHPATCRPLAV 180
 QY 181 EPGAAAASVSTTGGPPARAGADFOALPVGSSAAVAAPLGLQMLCTAPGAAVGHARBAR 240
 DB 181 EPGAAAASVSTTGGPPARAGADFOALPVGSSAAVAAPLGLQMLCTAPGAAVGHARBAR 240
 QY 181 EPGAAAASVSTTGGPPARAGADFOALPVGSSAAVAAPLGLQMLCTAPGAAVGHARBAR 240
 DB 181 EPGAAAASVSTTGGPPARAGADFOALPVGSSAAVAAPLGLQMLCTAPGAAVGHARBAR 240
 QY 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSRCTAS-TQSCNDLCEHFCEVNP 299
 DB 241 GAMDCSVENGGCEHACNAIPGARPCQCPAGALQADGSRCTAS-TQSCNDLCEHFCEVNP 299
 QY 300 DQPGSYSCMCTGYRLAADQHRCEVDVDCILPSPCPORCVNTQGFCHCYPNYDLVDG 359
 DB 300 DQPGSYSCMCTGYRLAADQHRCEVDVDCILPSPCPORCVNTQGFCHCYPNYDLVDG 359
 QY 301 DQPGSYSCMCTGYRLAADQHRCEVDVDCILPSPCPORCVNTQGFCHCYPNYDLVDG 360
 DB 301 DQPGSYSCMCTGYRLAADQHRCEVDVDCILPSPCPORCVNTQGFCHCYPNYDLVDG 360
 QY 360 ECVFVNDPCFRANCYOCQPLNQTSTYLCVCAEGFAPLPHBPRCOMFCNQTACPADCPN 419
 DB 360 ECVFVNDPCFRANCYOCQPLNQTSTYLCVCAEGFAPLPHBPRCOMFCNQTACPADCPN 419
 QY 361 ECVFVNDPCFRANCYOCQPLNQTSTYLCVCAEGFAPLPHBPRCOMFCNQTACPADCPN 420
 DB 361 ECVFVNDPCFRANCYOCQPLNQTSTYLCVCAEGFAPLPHBPRCOMFCNQTACPADCPN 420
 QY 420 TOASCECEGYILDDGFICTDIDECENGFGSGVCHNLPGTPECICGPDALARIHTGDC 479

Db	421	TOASCCECPBEgyILDDGFICTDIDECENGFCSGVCHNLPGTFECICGPDsALVRHIGTDC	480
Qy	480	DSGKVDGDDSGSGEPPTPGSTLTTPPAVGLVHSGLLIGISIASLCLVVALLALCHLR	539
Db	481	DSGKVDGDDSGSGEPPTPGSTLTTPPAVGLVHSGLLIGISIASLCLVVALLALCHLR	540
Qy	540	KKOGARAKMEYKCAPSKEVVLQHVRTERTPORL	574
Db	541	KKOGARAKMEYKCAPSKEVVLQHVRTERTPORL	575

Search completed: February 4, 2006, 04:27:57
Job time : 202 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 4, 2006, 04:28:12 ; Search time 45 Seconds
(without alignments)
1227.298 Million cell updates/sec

Title: US-10-725-013-2

Perfect score: 3203
Sequence: 1 MGVVLVGLNALAGLGGPPAP.....APSKVVLQHVRTERTPQL 574

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3172.5	99.0	575	1	THHUB
2	2113.5	66.0	577	2	thrombomodulin pre
3	1314	41.0	356	2	thrombomodulin - b
4	414.5	12.9	1574	2	MEGF6 protein - ra
5	411	12.8	1620	2	hypothetical prote
6	384	12.0	2871	2	fibrillin I - bovl
7	384	12.0	3002	2	fibrillin I precu
8	382	11.9	2871	2	fibrillin-1 precu
9	374.5	11.7	2907	2	fibrillin-2 precu
10	373.5	11.7	2918	2	fibrillin-2 precu
11	363	11.3	1184	2	fibrillin-2 precu
12	358.5	11.2	741	2	hypothetical prote
13	356.5	11.1	1221	2	fibulin-2 precursor
14	333	10.4	1712	2	fibulin-1 precursor
15	330.5	10.3	589	2	fibulin-1D precus
16	325	10.1	1394	2	transforming growt
17	324	10.1	689	2	fibulin, splice fo
18	324	10.1	712	2	fibulin 1, splice
19	323.5	10.1	1964	2	notch3 - mouse
20	315.5	9.9	2321	2	notch3 protein - h
21	312.5	9.7	798	2	hypothetical prote
22	310.5	9.7	601	2	fibulin 1 precursor
23	310.5	9.7	683	2	fibulin 1 precursor
24	308	9.6	1820	2	latent transformin
25	304	9.5	3507	2	hypothetical prote
26	303.5	9.5	685	2	fibulin, splice fo
27	302.5	9.4	705	2	fibulin, splice fo
28	300	9.4	1251	2	latent transformin
29	288	9.0	2437	2	transmembrane prot

30	286.5	8.9	2531	2	A46019	notch-1 protein -
31	285.5	8.9	2352	2	T30201	Notch homolog prot
32	284.5	8.9	2471	2	A49128	cell-fate determin
33	284	8.9	2703	1	A24420	notch protein - fr
34	283.5	8.9	2318	2	S45306	notch 3 protein -
35	281	8.8	387	2	I38449	extracellular prote
36	277.5	8.7	511	2	T17298	hypothetical prote
37	275	8.6	493	2	JC5621	epidermal growth f
38	273.5	8.5	2531	2	S18188	notch protein homo
39	270	8.4	2555	2	A40043	notch protein homo
40	263.5	8.2	1203	2	A49175	Notch B protein -
41	263.5	8.2	1217	1	EGMSWG	epidermal growth f
42	263	8.2	2531	2	T31070	notch homolog - se
43	257	8.0	624	2	A35844	Xorch protein - Af
44	254	7.9	254	2	I55476	growth potential
45	253.5	7.9	1133	1	EGRT	epidermal growth f

ALIGNMENTS

RESULT 1

THHUB
thrombomodulin precursor [validated] - human
C.Species: Homo sapiens (man)
C.Date: 31-Dec-1988 #sequence revision 12-May-1995 #text change 09-Jul-2004
C.Accession: A41442; A28307; A29680; A27073; JX0264; S38954
R.Shirai, T.; Shiojiri, S.; Ito, H.; Yamamoto, S.; Kusumoto, H.; Deyashiki, Y.; Maruyama
J. Biochem. 103, 281-285, 1988
A.Title: Gene structure of human thrombomodulin, a cofactor for thrombin-catalyzed activ
A.Reference number: A41442; MUID:88227901; PMID:2836377
A.Accession: A41442
A.Molecule type: DNA
A.Residues: 1-575 <SH>
A.Cross-references: UNIPROT:P07204; UNIPARC:UPI0000498FB; DDBJ:D00210; NID:G220126; PID
R.Jackman, R.W.; Beeler, D.L.; Fritze, L.; Soff, G.; Rosenberg, R.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 6425-6429, 1987
A.Title: Human thrombomodulin gene is intron depleted: nucleic acid sequences of the cDN
A.Reference number: A28307; MUID:8731765; PMID:2819876
A.Accession: A28307
A.Molecule type: mRNA
A.Residues: 1-472, 'A', 474-575 <JAC>
A.Cross-references: UNIPARC:UPI0000002BD; GB:J02973; NID:G339658; PIDN:AA61175.1; PID
R.Suzuki, K.; Kusumoto, H.; Deyashiki, Y.; Nishioke, J.; Maruyama, I.; Zushi, M.; Kawaha
EMBO J. 6, 1891-1897, 1987
A.Title: Structure and expression of human thrombomodulin, a thrombin receptor on endoth
A.Reference number: A29680; MUID:88004395; PMID:2820710
A.Accession: A29680
A.Molecule type: mRNA
A.Residues: 1-575 <SH>
A.Cross-references: UNIPARC:UPI00000498FB; GB:X05495; NID:G37123; PIDN:CAA29045.1; PID:G
A.Experimental source: lung endothelium
A.Note: part of this sequence, including the amino end of the mature protein, were deter
R.Wen, D.; Dittman, W.A.; Ye, R.D.; Deaven, L.L.; Majerus, P.W.; Sadler, J.E.
Biochemistry 26, 4350-4357, 1987
A.Title: Human thrombomodulin: complete cDNA sequence and chromosome localization of the
A.Reference number: A27073; MUID:88024950; PMID:2822087
A.Accession: A27073
A.Molecule type: mRNA
A.Residues: 1-472, 'A', 474-575 <WEN>
A.Cross-references: UNIPARC:UPI0000002BD; GB:M16552; NID:G339656; PIDN:AAB5908.1; PID
A.Experimental source: placenta
A.Note: parts of this sequence were determined by protein sequencing
R.Yamamoto, S.; Mizoguchi, T.; Tamaki, T.; Ohkuchi, M.; Kimura, S.; Aoki, N.
J. Biochem. 113, 433-440, 1993
A.Title: Urinary thrombomodulin, its isolation and characterization.
A.Reference number: JX0264; MUID:93293792; PMID:8390446
A.Accession: JX0264
A.Molecule type: protein, mRNA
A.Residues: 19-472, 'A', 474-486 <YAM>
A.Cross-references: UNIPARC:UPI000017341
A.Experimental source: urine
A.Note: the urinary form appears to be identical with that circulating in plasma

R;Gerlitz, B.; Haesell, T.; Vlahos, C.J.; Parkinson, J.F.; Bang, N.U.; Grinnell, B.W.
 Biochem. J. 295, 131-140, 1993
 A>Title: Identification of the predominant glycosaminoglycan-attachment site in soluble
 serine.
 A;Reference number: S38954; MUID:94029900; PMID:8216207
 A;Accession: S38954
 A;Molecule type: protein
 A;Residues: 475-491, 'X', 493-494 <GER>
 A;Cross-references: UNIPARC:UPI0000173342
 A;Note: the residue designated 'X' was determined to be a Ser with covalently bound chon
 R;Meininger, D.P.; Komives, E.A.
 submitted to the Brookhaven Protein Data Bank, September 1995
 A;Reference number: A67369; PDB:1ZQ
 A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
 R;Tulinsky, A.; Mathews, I.I.
 submitted to the Brookhaven Protein Data Bank, August 1994
 A;Reference number: A52804; PDB:1HUT
 A;Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 426-442
 R;Hrabal, R.; Komives, E.A.; Ni, F.
 submitted to the Brookhaven Protein Data Bank, November 1995
 A;Reference number: A65583; PDB:1FGD
 A;Contents: annotation; conformation by (1)H-NMR, residues 427-444
 R;Hrabal, R.; Komives, E.A.; Ni, F.
 Protein Sci. 5, 195-203, 1996
 A>Title: Structural resiliency of an EGF-like subdomain bound to its target protein, the
 A;Reference number: A58595; MUID:96276211; PMID:8745396
 A;Contents: annotation; conformation by (1)H-NMR
 C;Genetics:
 A;Gene: GDB:THBD
 A;Cross-references: GDB:119613; OMIM:188040
 A;Map position: 20p11.2-20p11.2
 A;introns: #status absent
 C;Complex: homodimer, urinary form
 C;Function:
 A;Description: inhibits thrombin activation of fibrinogen; cofactor for thrombin activat
 A;Pathway: blood coagulation moderation
 A;Note: the membrane-bound form is located on the endothelium luminal surface of arterie
 A;Note: thrombin complexed with the membrane-bound form is subject to endocytosis
 C;Superfamily: thrombomodulin; C-type lectin homology; EGF homology
 C;Keywords: anticoagulant; beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coag
 e protein
 F;1-18/Domain: signal sequence #status predicted <STG>
 F;19-575/Product: thrombomodulin, membrane-bound form #status predicted <MAT>
 F;19-513/Domain: extracellular #status predicted <EXT>
 F;19-486/Product: thrombomodulin, urinary form #status experimental <MAU>
 F;24-167/Domain: C-type lectin homology <LCH>
 F;177-199/Region: PEST sequence
 F;201-233/Region: PEST sequence
 F;245-280/Domain: EGF homology <EG1>
 F;288-323/Domain: EGF homology <EG2>
 F;328-362/Domain: EGF homology <EG3>
 F;369-404/Domain: EGF homology <EG4>
 F;408-439/Domain: EGF homology <EG5>
 F;445-480/Domain: EGF homology <EG6>
 F;485-513/Region: PEST sequence
 F;517-539/Domain: transmembrane #status predicted <TMN>
 F;540-575/Domain: intracellular #status predicted <INT>
 F;47,115,116,382,409/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;174,225,411,504/Binding site: carboxylate (Thr) (covalent) #status predicted
 F;245-256,252-265,267-280,288-296,292-308,310-323,329-340,336-349,351-362,369-378,374-38
 F;334,458/Binding site: carboxylate (Ser) (covalent) #status predicted
 F;342/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
 F;490,492/Binding site: chondroitin sulfate (Ser) (covalent) (partial) #status experimen

Query Match 99.0%; Score 3172.5; DB 1; Length 575;
 Best Local Similarity 99.3%; Pred. No. 7.3e-182;
 Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MGVVILALALAGIGFPAAPAPPOGSGSCVHDDPAPYAPGPATFLNSQICDGLRGHLM 60
 DB 1 MGVVILALALAGIGFPAAPAPPOGSGSCVHDDPAPYAPGPATFLNSQICDGLRGHLM 60

QY 61 TVRSSVAADVLSILNDGSGVRRRLWIGLQLPFGCGDPKRLGPGVMTGDNNTSYS 120

DB 61 TVRSSVAADVLSILNDGSGVRRRLWIGLQLPFGCGDPKRLGPGVMTGDNNTSYS 120
 QY 121 RMARLDLNGADPLCGPLCVAVSAATVPSEPIWEEQCEKADGFLCEHFPATCRPLAV 180
 DB 121 RMARLDLNGADPLCGPLCVAVSAATVPSEPIWEEQCEKADGFLCEHFPATCRPLAV 180
 QY 181 EPGAAAAAVSTTGTTPFAARADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHMARBP 240
 DB 181 EPGAAAAAVSTTGTTPFAARADFOALPVGSSAAVAPLGLQLMCTAPPGAVQGHMARBP 240
 QY 241 GAMDCSVENGGCEHACNAIPGAPPCQCPAGAALOADGSCFAS-TQSCNDLCSEHCVENP 299
 DB 241 GAMDCSVENGGCEHACNAIPGAPPCQCPAGAALOADGSCFAS-TQSCNDLCSEHCVENP 299
 QY 300 DQPGSGSCMCEGTGYRLAADQHRCEVDVDCILEPSPCPCRVNTQGFECCHCYPNYDLVDG 359
 DB 301 DQPGSGSCMCEGTGYRLAADQHRCEVDVDCILEPSPCPCRVNTQGFECCHCYPNYDLVDG 359
 QY 360 ECVPEVDPCEPANCERYCQPLNQTSTYLCVCAEGFAPTPHEHRCMPFCNQTACPADCDPN 419
 DB 361 ECVPEVDPCEPANCERYCQPLNQTSTYLCVCAEGFAPTPHEHRCMPFCNQTACPADCDPN 419
 QY 420 TQASCEGEGYILDDGFLCTDIDECENGFGSGVCHNLPGTFECICGPDALARIHGTDC 479
 DB 421 TQASCEGEGYILDDGFLCTDIDECENGFGSGVCHNLPGTFECICGPDALARIHGTDC 479
 QY 480 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLAILCHLR 539
 DB 481 DSGKVDGSDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLAILCHLR 539
 QY 540 KKQGAARAKMEYKCAAPSEKVVLLQHVTERTPORL 574
 DB 541 KKQGAARAKMEYKCAAPSEKVVLLQHVTERTPORL 574

RESULT 2
 A60501
 thrombomodulin precursor - mouse
 N:Alternate names: fetomoduulin
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
 C;Accession: S08488; A32001; A60501
 R;Dittman, W.A.; Majerus, P.W.
 Nucleic Acids Res. 17, 802, 1989
 A>Title: Sequence of a cDNA for mouse thrombomodulin and comparison of the predicted mou
 A;Reference number: S08488; MUID:89128454; PMID:2536925
 A;Accession: S08488
 A;Molecule type: mRNA
 A;Residues: 1-577 <DIR>
 A;Cross-references: UNIPROT:P15306; UNIPARC:UPI00000197C; EMBL:X14432; NID:954781; PIDN
 R;Dittman, W.A.; Kumada, T.; Sadler, J.E.; Majerus, P.W.
 J. Biol. Chem. 263, 15815-15822, 1988
 A>Title: The structure and function of mouse thrombomodulin. Phorbol myristate acetate s
 A;Reference number: A32001; MUID:89008498; PMID:2844823
 A;Accession: A32001
 A;Molecule type: mRNA
 A;Residues: 97-577 <DIR>
 A;Cross-references: UNIPARC:UPI0000176503; GB:J04060
 R;Imada, S.; Yamaguchi, H.; Nagumo, M.; Katsuyamagi, S.; Iwasaki, H.; Imada, M.
 Dev. Biol. 140, 113-122, 1990
 A>Title: Identification of fetomoduulin, a surface marker protein of fetal development, a
 A;Reference number: A60501; MUID:90292331; PMID:2162790
 A;Accession: A60501
 A;Molecule type: protein
 A;Residues: 19-22,330-343,479-489,545-555,562-575 <IMA>
 A;Cross-references: UNIPARC:UPI0000174DF0; UNIPARC:UPI0000176504; UNIPARC:UPI0000176505;
 C;Comment: Thrombomodulin binds to and internalizes with thrombin. It is also a cofactor
 C;Superfamily: thrombomodulin; C-type lectin homology; EGF homology
 C;Keywords: anticoagulant; membrane protein; phosphoprotein; receptor
 F;24-165/Domain: C-type lectin homology <LCH>
 F;244-279/Domain: EGF homology <EG1>
 F;287-322/Domain: EGF homology <EG2>

F:328-361/Domain: EGF homology <EG3>
 F:368-403/Domain: EGF homology <EG4>
 F:407-438/Domain: EGF homology <EG5>
 F:444-479/Domain: EGF homology <EG6>

Query Match 66.0%; Score 2113.5; DB 2; Length 577;
 Best Local Similarity 67.0%; Pred. No. 8.3e-119;
 Matches 388; Conservative 53; Mismatches 129; Indels 9; Gaps 5;

QY 1 MLGVTLALALAGFPAPAPPOGSGQVHDFCALPYGPATLNASQICDGLRGLH 60
 DB 1 MLGTFPLVLAIPASIGLSALALQPTGSCVHBCFALFQGPATLNASQACORLQGHM 60
 QY 61 TVRSSVADVI SLILNDG- GVGRRRLWIGLQLPCCGPKRIGLRGFWYTGDNNTSY 119
 DB 61 TVRSSVADVI SLILSGSMIDG- WIGLQLPCCGDDPHLGRGFWYTGDNNTSY 117
 QY 120 SRMARLDLNGAPLCPPLCVANSAEATVPSEPIWEEQCEVADGFLCEPHPATCPDIA 179
 DB 118 SRMARLNDOTAPLCPPLCVATSTATEAAGBEPAMEKECEETQGLCEFYFTASCRLT 177
 QY 180 VEP- GAAAASITVGFEPFARGADFOALPVGSSAAVAPLGLQMLCTAPGAGVQHMARE 238
 DB 178 VMTDPEAAHISTNTTFVGSADFOPLPVGSSAAVEPLGLGLVCRAPPGTSBGHAME 237
 QY 239 APGAMDCSVENGGEHACNAIPGARPCQCPAGALQADGRSCTAS- TQSCNDLCEHFCVP 297
 DB 238 ATGAMNCSVENGGCEYLGNRSTNEPRCLCPRDMDLQADGRCARVVGSCNHELCEHFCVS 297
 QY 298 NPDPGSGSCMCEGYRLAADQHRCEVDCTLEBSPCPQRCVNTGGFECPCPNYDLV 357
 DB 298 NAEVPGSGSCMCEGYQLAADGHRCEVDCKQGNPQPCVMTKGFCECYDGYELV 357
 QY 358 DGECEPDPGCFRANCEYQOCLINTSYLCVCAEFAPRIPHEPRHCOMFNCQTACPADCD 417
 DB 358 DGECEVLDPCFGSCFQCPVSTDRCTICAPFAPKPBPHKCEMFCEMTSGPADCD 417
 QY 418 PNTQASCEPEGYIILDDFICTDIDECENGGFCGVCHNLPGTFECICGPSPALARIHGT 477
 DB 418 PNTPTVCECPGFIIDBSGVCITDIDECQSGCFSTSECNPFQSGVECTICGPPTALAGQISK 477
 QY 478 DCDGSKV- DGDGSGSGEPSPPTSTLTPPAVLVHSGLLIGISIASLCTVVALLAT 534
 DB 478 DCDP1PVREDTKEBEGSEPPVSPTPGSPTRPSPARPHSGVLIGISIASLCTVVALLAT 537
 QY 535 LCHIRKKGARARAMEYKCAAPSKENVLQHVRTERTPQR 573
 DB 538 LCHIRKKGARARAMEYKCAASAKEVYLQHVRTDRTLOK 576

RESULT 3

A25918
 thrombomodulin - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
 C:Accession: A25918
 R:Juckman, R.W.; Beeler, D.L.; Vandewater, L.; Rosenberg, R.D.
 Proc. Natl. Acad. Sci. U.S.A. 83, 8834-8838, 1986
 A:Title: Characterization of a thrombomodulin cDNA reveals structural similarity to the
 A:Reference number: A25918; MUID:87067408; PMID:3024152
 A:Accession: A25918
 A:Molecule type: mRNA
 A:Residues: 1-356 <JUG>
 A:Cross-references: UNIPROT: P06579; UNIPARC: UP1000013732F; GB: M14657; NID: g163762; PIDN:
 C:Superfamily: thrombomodulin; C-type lectin homology; EGF homology
 C:Keywords: transmembrane protein
 F:21-56/Domain: EGF homology <EG1>
 F:64-97/Domain: EGF homology <EG2>
 F:103-136/Domain: EGF homology <EG3>
 F:143-178/Domain: EGF homology <EG4>
 F:182-213/Domain: EGF homology <EG5>
 F:219-253/Domain: EGF homology <EG6>

Query Match 41.0%; Score 1314; DB 2; Length 356;
 Best Local Similarity 65.0%; Pred. No. 2.2e-71;
 Matches 232; Conservative 42; Mismatches 67; Indels 16; Gaps 7;

QY 229 GAVGHMARREAPGAWDCSVENGGEHACNAIPGARPCQCPAGALQADGRSC- TASTOSC 287
 DB 5 GETBERMREAPGAWACVBERGGCOHECKGASAGSNCLCPADALQADGRSGCLPAEHPC 64
 QY 288 NDLCHEFCVPPDDGSGYSCMCEGYRLAADQHRCEVDCTLEBSPCPQRCVNTGGFPE 347
 DB 65 HOLCEHFC- HHLGKANTTICIEAGYQLAADQHRCEVDCTLEBSPCPQRCVNTGGFPE 122
 QY 348 CHCEPNYDLVDBCEPAPDPCFRANCEYQOCLINTSYLCVCAEFAPRIPHEPRHCOMFC 407
 DB 123 CHCEPNYDLVDBCEPAPDPCFRANCEYQOCLINTSYLCVCAEFAPRIPHEPRHCOMFC 182
 QY 408 NOTACPADCDPNTQASCEPEGYIILDDFICTDIDECENGGFCGVCHNLPGTFECICGP 467
 DB 183 NOTSCPADCDPHYPTICRCEPGYIILDSGTCITDINECDT- NICPQCHNLPGTFECICGP 241
 QY 468 DSALAHITGTDGSGKV- DGDGSGSGEPSPPTSTLTP- PAVLHSGLL 517
 DB 242 DSALSGQIGIDCDPTQVNERGTPEDYG- GSGEPVSPTRGATAPSPAPAGPLHSGVL 299
 QY 518 IGISIASLCTVVALLATLCHIRKKGARARAMEYKCAAPSKENVLQHVRTERTPQR 574
 DB 300 VGISIASLCTVVALLATLCHIRKKGASRGLLEKCGVPAEMLVQVKTERTPQKL 356

RESULT 4

MEGF6 protein - rat
 T13954
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T13954
 R:Nakajima, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
 Genomics 51, 27-34, 1998
 A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
 A:Reference number: Z14126; MUID:98360089; PMID:9639030
 A:Accession: T13954
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1574 <NAK>
 A:Cross-references: UNIPROT: O08281; UNIPARC: UP10000043BEE; EMBL: AB011532; NID: g3449293;
 A:Experimental source: Strain Sprague-Dawley; brain
 A:Gene: MEGF6

Query Match 12.9%; Score 414.5; DB 2; Length 1574;
 Best Local Similarity 34.2%; Pred. No. 2.8e-17;
 Matches 104; Conservative 28; Mismatches 101; Indels 71; Gaps 17;

QY 224 CTAPPG- AVQGHMARREAPGAWDCSVENGGEHACNAIPGARPCQCPAGALQADGRSCTA 282
 DB 147 CRCEPGYQLQGD- GKTQGDVDECRANHGCGQHRCVNTPGSLGCKXGFRHLHTDGRCTLA 205
 QY 283 STQSC- NDLCHEFCVP- NPDQPGSYSCM- 308
 DB 206 -ISSCTLVANGCQHQCVQLTVTQHRCCQRPQYQLQEDGRRRCVRSFPAEAGGGMHCQ 264
 QY 309 -CEGYRLADQHRCEVDCTLEBSPCPQRCVNTGGFECPCPNYDL- VDG 359
 DB 265 IRLGLAHGCHPQYQLADRKTCEDVDCLAGLQAGHCAGCLNTQGSFKCVCHAGYELGADG 324
 QY 325 RQCRIMEIIVNSCEANGGCSHCSH- TSTGPLCTCPRGV- ELDEQKTCIDIDD 378
 DB 360 -EC- VEPVDPGFRAN- CEYQOCLINTSYLCVCAEFAPRIPHEPRHCOMFC- 407
 QY 408 -NOTACPADCDPNTQ- SCEPEGYIIL- DGTCTDIDECENG- GFCGVCNHLGTF 461
 DB 379 CAUSPCQOAC- ANTPEGYCSCPAGYRLNTDGGCERDVBCASGHGCGCEHHCNLAGSP 437
 QY 462 ECIC 465

Db 438 QCFC 441

RESULT 5

hypothetical protein Y64G10A.f - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T27283

R/Accession: R
submitted to the EMBL Data Library, September 1999

A/Reference number: Z20336

A/Accession: T27283

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1620 <WTL>

A/Cross-references: UNIPARC:UPI000017BCB4; EMBL:AL110498; NID:e1542303; PIDN:CB54471.1;

A/Experimental source: clone Y64G10A

C/GeneticB:

A/Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 7

Query Match 12.8%; Score 411; DB 2; Length 1620;

Best Local Similarity 25.9%; Pred. No. 4.6e-17;

Matches 142; Conservative 47; Mismatches 197; Indels 162; Gaps 25;

119 YSRMARLNLNGAPLCGPLCVAVSAE-----ATPSEPIWEEQCE--VKADFLCEF 169

Db 56 YLRPARFRGRGSKCCLLRQVQANGADLCHNGCTVPEBHNDNEQVCECPGFTGAKQY 115

QY 170 HFPATCRPLAVEPGAAAAAASITVGTTPPAARGADFOALPVGSSAAVAPLGLQMLCTAPRG 229

Db 116 D-ANEC--MANNGGCEHCVN-TIGTY-----CRCWPG 145

QY 220 AVCGMAEAEAGAMCSVENGGCEHACVAIPGARPCQCPAGALADRSCTASTQSC-- 287

Db 146 FELSGDNGTCSDDIDCAVNSGCSDRCVNSPGFRCDCSDLYLHADGTGKATV-SCST 204

QY 288 -NDLCEHFVPPNPDPGSGYSQWCEGYRLADQHRCEVDVDCILEBSPCPCRCVNTQCGF 346

Db 205 DNGGCEHC-ENDSNGEYRCKCRGVFKLSKSKSCQRPDPFDKGGCQNNCTNNHRA 263

QY 347 ECHCYPNYDL-VDGCEVPEVPCFRAN-CEYQCPQLNQTSYLCVACGAPAPVPHPHRCQ 404

Db 264 QCCYPRGHLSDYDRSCVDIDECANNGCEHCENYKGT-YRCKREGY-QLGRDGRICE 321

QY 405 MF-----CNGTRACPADC--DPTQASCECPBGTYL----- 432

Db 322 EMLGGCQVNGGCGQHDYDQPDGHHVCKCRNGYILANDQKLCNDNISTVIHARAPRLMDS 381

QY 433 -----DDGF-----ICTDIDEC-ENGFCGSGVCH 455

Db 382 YETVTCVPTDITLTKLCHMLDSDGAVQCFCDYGLIDLSKFCQDINECHENNDDSCQICV 441

QY 456 NLPGTEFCICGPDLSLAHIGT-----DCDSKVDG-----DSGSGEPSPPTGSLTY 505

Db 442 NLASGVCEQCKRQFPLMKDRKTCEDISESSN--NGGCEQICSNQEGGVMGSCERGFELS 499

QY 506 PPANG-----LVHSGLLIGTSLASLCLVALLMLLCHLRKKGAAAR-----AKM 549

Db 500 EDGHSCHDMNECLINNG-----GCAQLC-----KNRKGSRRCQCFAGYILAMD 542

QY 550 EYKCAAPS 557

Db 543 EKSCVAAS 550

RESULT 6

A55567

fibrillin 1 - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C/Accession: A55567

R/Title: D.U.; Li, L.; Potter, K.A.; Womack, J.; Byers, P.H.

Genomics 23, 480-485, 1994

A/Title: Sequence of the coding region of the bovine fibrillin cDNA and localization to

A/Reference number: A55567; MUID:95137597; PMID:7835900

A/Accession: A55567

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-2871 <TIL>

A/Cross-references: UNIPROT:P98133; UNIPARC:UPI0000055AD2; GB:L28748; NID:9508427; PIDN:J

C/Superfamily: fibrillin; EGF homology

F.1201-1236/Domain: EGF homology <EGF>

Query Match 12.0%; Score 384; DB 2; Length 2871;

Best Local Similarity 29.3%; Pred. No. 3e-15;

Matches 129; Conservative 32; Mismatches 129; Indels 150; Gaps 25;

244 DCSYNGGCEHACVAIPGARPCQCPAGALADRSCTASTQSCNDLCEHFVNP----- 299

Db 1200 ECSIANGGCEHACVAIPGARPCQCPAGALADRSCTASTQSCNDLCEHFVNP----- 1250

QY 300 -----DQGSYSQWCEGYRLADQHRCEVDVDCILEBSPC-PQRCVNTQCGFCHCYPN 353

Db 1251 GGQCTNIRGEYRCICVDGFMASEDMKTCVDVNECDLNPNICLSGTCEHTKGSFICHCDMG 1310

QY 354 YDLVDGE--CYEPVDP--FRANCEYQCPANQ--SYLCVABEFA-----PIPH 398

Db 1311 YSGKKGKGTCTD-INCEIGAHNCDRAHACTNTAGSFKSCSPWIGDGIKCTDLDECSN 1369

QY 399 EPHRCQWFCNQDTACPADCPNTQAS--CECEGYTLDDGFICTDIDEC-EN----- 446

Db 1370 GTMCSQH-----ADC-KRTMGSYRLCLCEGY-TGSGFTCTDDESENLNCGNQ 1420

QY 447 ---GGF-----GVCNLPPTRECTIGPDSALAR 473

Db 1421 LNAFGYRCCEDMGFVPSADKACEDIDECSLPNIQVGTGCHNLPLGRCCBCEIGYELDR 1480

QY 474 HIG-----TDCNSGR-VQGDGSGSEBPPSPPTGSLTPPANGLV--HSG----- 515

Db 1481 SGGNCTDVNECLDPTTICSGACVNTPGSYTDCDPPD---FELNTRGCVDTNSGNCYL 1536

QY 516 -----LTIQISIASLCLVALLMLLCHLRKKGAAARA-----KMEYKC 553

Db 1537 DIRPBGNDGDTACNSIEIGVYSKASC-----CSLGRAMKGRPCELCPVNTSEYKI 1587

QY 554 AAPSKE-----VTLQHV 565

Db 1588 LCPGEGFRPMPITVYILEDI 1607

RESULT 7

A47221

fibrillin 1 precursor - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 02-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 31-Dec-2004

C/Accession: A47221; I54355; S17064; I59574; S17062; S62111; A34198

R/Corson, G.M.; Chabberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.

Genomics 17, 476-484, 1993

A/Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structure

A/Reference number: A47221; MUID:94010947; PMID:7691719

A/Accession: A47221

A/Molecule type: mRNA

A/Residues: 1-337; T, 339-1029 <COR>

A/Cross-references: UNIPROT:P35555; UNIPROT:Q15972; UNIPARC:Q9NP01; UNIPARC:UPI000017651

A/Reference number: I54355; MUID:93372860; PMID:8364578

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 132-3002 <PBR>

A/Cross-references: UNIPARC:UPI0000055AD1; GB:LI3923; NID:9306745; PIDN:AA802036.1; PID:

R.Maehlen, C.L.; Corson, G.M.; Maddox, B.K.; Gianville, R.W.; Sakai, L.Y.
Nucleus 352, 334-337, 1991
A>Title: Partial sequence of a candidate gene for the Marfan syndrome.
A/Accession: S17064; MUID:91304568; PMID:1852207
A/Accession: S17064
A/Molecule type: mRNA
A/Residues: 1030-3002 <MAS>
A/Cross-references: UNIPARC:UPI0000176517; EMBL:X63556
R.Dietz, H.C.; Valle, D.; Franccomano, C.A.; Kendzior, R.J.
Science 259, 680-683, 1993
A>Title: The skipping of constitutive exons in vivo induced by nonsense mutations.
A/Reference number: 159574; MUID:93157831; PMID:8430317
A/Accession: S19574
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 2217-2288, '1', 2290-2325 <REBS>
A/Cross-references: UNIPARC:UPI000006FF66; GB:S54426; NID:9264860; PIDN:AAB25244.1; PID:
Rilee, B.; Godfrey, M.; Vitale, E.; Horii, H.; Mattei, M.G.; Sarfraz, M.; Tsipouras, P.
Nucleus 352, 330-334, 1991
A>Title: Linkage of Marfan syndrome and a phenotypically related disorder to two different
A/Reference number: S17062; MUID:91304567; PMID:1852206
A/Accession: S17062
A/Molecule type: mRNA
A/Residues: 'VAVTVFRLSYKML', 944-1444 <LEB1>
A/Cross-references: UNIPARC:UPI0000072A79; EMBL:X62008; NID:931398; PIDN:CAH56534.1; PID:
A/Accession: S62111
A/Molecule type: Protein
A/Residues: 1166-1176, 'X', 1178-1180, 'D', 1182-1185 <LEB2>
A/Cross-references: UNIPARC:UPI0000176518
R.Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Gianville, R.W.
J. Biol. Chem. 264, 21381-21385, 1989
A>Title: Connective tissue microfibrils. Isolation and characterization of three large F
A/Reference number: A34198; MUID:90078246; PMID:2512293
A/Accession: A34198
A/Molecule type: Protein
A/Residues: 565-575, 1890-1892, 'T', 1894-1900 <MAD>
A/Cross-references: UNIPARC:UPI0000176519; UNIPARC:UPI000017651A
C/Comment: Fibrillin is a major component of elastin-associated microfibrils.
C/Genetics:
A/Gene: GDB:FBN1
A/Cross-references: GDB:127115; OMIM:134797; OMIM:154700
A/Map position: 15q21.1-15q21.1
A/Intons: 2236/1, 2258/1, 2297/1
C/Superfamily: EGF homology
C/Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein; M
F:1-3002/Product: fibrillin (5'-region exon A splice form) (fragment) #status predicted
F:132-3002/Product: fibrillin (5'-region exon C splice form) #status predicted <MARC>
F:1332-1367/Domain: EGF homology <EGF2>
F:1457-1492/Domain: EGF homology <EGF2>
F:2262-2295/Domain: EGF homology <EGF1>

Query Match 12.0%; Score 384; DB 2; Length 3002;
Best Local Similarity 29.0%; Pred. No. 3.1e-15;
Matches 130; Conservative 28; Mismatches 124; Indels 166; Gaps 25;

QY 244 DCSYENGGCEHAICAIIPGAPCCQCPAGALADGSCASTOSGNDLCEHFCEVNP----- 299
DB 1331 ECSIIMNGCETFCINSESYECSCQPFALMPDQSC-----DIE--CEDNPNICD 1381
QY 300 -----DQGSYSICMCTGYRLADQHRCEVDVDCILPEPSC--PQRCVNTQGGFCHCYPN 353
DB 1382 GGQCTNIPGEYRCLCYDFMASEDMKTCVDVNECDLNPNICLSTGCENTKGSFICHDMG 1441
QY 354 YDVLVDE--CYEPVDP--FRANCEYQCPINQ--SYLCVCAEGFA-----PIPH 398
DB 1442 YSGKKGKGTCTD--INCEIGAHNGCKAVCTNTAGSFKSCSPGIMGIGIKCTDLDECSN 1500
QY 399 EPHRCQMFQCTACPADCPNTQAS--CECEGYILDDGFICTDIDEC--EN----- 446
DB 1501 GTNHCQH-----ADC-KRTMGSYRCLCKEGY--TGSGFTCTDLDECSNLANCGNQC 1551
QY 447 ---GGF-----GS-----GVCNLPGTFEICGPDALAR 473

DB 1552 INAPGRCBCDMGFTVPADKACEDIDECSLPNICVFETCNLPGLFRCECEIGYELDR 1611
QY 474 HIG-----TDGSKVYDGDGSGSEBPPTPGS-----TLTPPAVGLV- 512
DB 1612 SGQNCITVNECDLPPTTCSGNV-----TGSYICDQPPPELNPTRVGCVD 1659
QY 513 -HSG-----LLIGISIASLCLVALLALCHLRKQGA-----A 545
DB 1660 TRSGNCYLDIPRGDNGDTAGSNEIGVSVKASCC-----CSLGAWGTPEMCPA 1710
QY 546 RAKMEYKCAAPSK-----VVLQHV 565
DB 1711 VNTSEYKILCPQGBGFRRNPITVLEDT 1738

RESULT 8
A55624
fibrillin-1 precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C/Accession: A55624
R.Yin, W.; Smiley, E.; Garmiller, J.; Sanguinetti, C.; Lawton, T.; Pereira, L.; Ramirez,
J. Biol. Chem. 270, 1798-1806, 1995
A>Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin ge
A/Reference number: A55624; MUID:95130561; PMID:7829516
A/Accession: A55624
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-2871 <YIN>
A/Cross-references: UNIPROT:Q61554; UNIPARC:UPI00000289B6; GB:L29454; NID:9575509; PIDN:
C/Genetics:
A/Gene: Fbn-1
C/Superfamily: fibrillin; EGF homology
F:1201-1236/Domain: EGF homology <EGF>

Query Match 11.9%; Score 382; DB 2; Length 2871;
Best Local Similarity 27.8%; Pred. No. 4e-15;
Matches 135; Conservative 31; Mismatches 148; Indels 172; Gaps 25;

QY 212 SAAVAIPGL-----QLMCTPRGAVGQHMAREARGAMDGVENGGCEHAICAIIPGAPPC 265
DB 1162 SANLCPIHRCVNLIGKYQACANPQYHPTDRLFCVDIDECISIMNGCCTFTNSDGSYEC 1221
QY 266 QCPAGALADGSCASTOSGNDLCEHFCEVNP-----DQGSYSICMCTGYRLA 316
DB 1222 SCQGFALMPDQSCITDQ-----CEDNPNICDGGCTNIPGEYRCLCYDFMAS 1272
QY 317 ADQHRCEVDVDCILPEPSC--PQRCVNTQGGFCHCYPNYDLVDE--CYEPVDP--FRA 371
DB 1273 EDMKTCVDVNECDLNPNICLSTGCENTKGSFICHDMGYSKKKGTGCTD--INCEIGAH 1331
QY 372 NCEYQCPINQ--SYLCVCAEGFA-----PIHBPFRQMFQCTACPADCPNT 420
DB 1332 NCGHNAVCTNTAGSFKSCSPGMIGDIKCTDLDECSNHTMCSQH-----ADC-KNT 1383
QY 421 QAS--CECEGYILDDGFICTDIDEC--EN-----GGF----- 449
DB 1384 MGSYRCLCKQDY--TGSGFTCTDLDECSNLANCGNQLNAPGYSRCBCEMGFTVPSADGK 1442
QY 450 -----CS-----GVCNLPGTFEICGPDALARHIG-----TDGSGKV 484
DB 1443 ACEDIDECSLPNICVFETCNLPGLFRCECEIGYELDRSGNCTVNECDLPPTTCSGNC 1502
QY 485 DGDGSGGSEBPPTPGS-----TLTPPAVGLV--HSG----- 515
DB 1503 VN-----TPGSYICDQSPDELPTRVGVCTDTSAGCNLYNIRPGDNGDTACS 1550
QY 516 --LLIGISIASLCLVALLALCHLRKQGA-----ARAKMEYKCAAPSK----- 559
DB 1551 NEIGVSVKASCC-----CSLGAWGTPELCPVNTSEYKILCPQGBGFRRNPIT 1601
QY 560 VVLQHV 565

RESULT 9

A57278
fibryllin-2 precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C:Accession: A57278
R:Zhang, H.; Hu, W.; Ramirez, F.
J. Cell Biol. 129, 1165-1176, 1995
A>Title: Developmental expression of fibrillin gene suggests heterogeneity of extracellular matrix
A:Reference number: A57278; MUID:95263670; PMID:7744963
A:Accession: A57278
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2907 >ZHA>
A:Cross-references: UNIPROT:Q61555; UNIPARC:UPI00000289B9; GB:I39790; NID:G762830; PIDD:
C:Superfamily: fibrillin; EGF homology
F:1239-1274/Domain: EGF homology <EGF1>
F:2488-2523/Domain: EGF homology <EGF>

Query Match 11.7%; Score 374.5; DB 2; Length 2907;
Best Local Similarity 33.0%; Pred. No. 1.1e-14;
Matches 102; Conservative 24; Mismatches 92; Indels 91; Gaps 18;

Dy 244 DCSVENGGCEACNAIPGARPCQCAGALQADGRCTASTQTSCNDLCEHFCVNPDP---300
 :
Db 1238 ECMINNGCGDQGTNSBSYSGSEGYALMPDGRSA-----DIDE--CENNPDI CD 1288
 :
Oy 301 -----QGTSICMCETGYRLAADQRCEVDYDDCLLESPCP-QRCVNTQGFECYCYPN 353
 :
Db 1289 GGQCTNIGEYKLCYDFPFMASMDKTCIDVNECDLPNIIMPFGCENTKTGSFLCHQLG 1348
 :
Oy 354 YDIVDGE--CYEPVPCC--FRANCEYGCQPLN-QSYLCVCAGEPA-----PIPH 398
 :
Db 1349 IYSVKKGTTGCTD-VDECI GAHNCDMHASCINVPESFKCSREBGVANGIKCIDLBECAN 1407
 :
Oy 399 EPHRCOMCNQACPADCPDPTQAS--CECEPGYLDDGFICTIDE-----CENG-- 447
 :
Db 1408 GTHQCSI-----NAQC-VITPGRYRCABSEG- TGDFGFCSDVDCAENTNL CENGOC 1458
 :
Oy 448 -----GF-----CS-----GVCHNLPGTFECICGPDSALAR 473
 :
Db 1459 LNVPGAHYCEGMGTPASDSRSCDDIDEGSFQNICVFHCNNLPQMWHICIDOGYEILDR 1518
 :
Oy 474 HIG--TDCD 480
 :
Db 1519 TGNCTDID 1527

RESULT 10

A54105
fibrillin-2 precursor - human
C:Species: Homo sapiens (man)
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: A54105; S17063; S31101
R:Zhang, H.; Apfelroth, S.D.; Hu, W.; Davis, E.C.; Sangunietti, C.; Bonadio, J.; Mecham,
J. Cell Biol. 124, 855-863, 1994
A>Title: Structure and expression of fibrillin-2, a novel microfibrillar component preferentially expressed in cartilage
A:Reference number: A54105; MUID:94165150; PMID:1820105
A:Accession: A54105
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-2818 >ZHA>
A:Cross-references: UNIPROT:P35556; UNIPARC:UPI000017651B; GB:U032272
R:Lee, B.; Godfrey, M.; Vitale, E.; Horii, H.; Mattei, M.G.; Sarfarazi, M.; Tsipouras, P.
Nature 352, 330-334, 1991
A>Title: Linkage of Marfan syndrome and a phenotypically related disorder to two different genes
A:Reference number: S17062; MUID:91304567; PMID:1852206
A:Accession: S17063
A:Molecule type: mRNA
A:Residues: 752-1489, 1791, 'GS', 1794-1796, 'OLT', 1922-1923, 'LD', 1926, 'P', 1928 <LEE>

A:Cross-references: UNIPARC:UPI000017651C; EMBL:X62009
R.Miliewicz, D.M.
Submitted to the EMBL Data Library, December 1992
A:Reference number: S31101
A:Accession: S31101
A:Molecule type: mRNA
A:Residues: 752-1407, 'R', '1409-1489, 1791, 'GS', '1794-1796, 'QU', '1922-1923, 'LD', '1926, 'P', '192
A:Cross-references: UNIPARC:UPI000000069B; EMBL:X62009
C:Genetics:
A:Gene: GDB:FBN2
A:Cross-references: GDB:128122; OMIM:121050
A:Map position: 5q23-5q31
C:Superfamily: fibrillin; EGF homology
C:Keywords: extracellular protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-2918/Product: fibrillin-2 #status predicted <MNT>
F:1245-1280/Domain: EGF homology <EGF1>
F:1970-2013/Domain: EGF homology <EGF>

Query Match 11.7%; Score 373.5; DB 2; Length 2918;
Best Local Similarity 29.9%; Pred. No. 1.3e-14;
Matches 118; Conservative 34; Mismatches 124; Indels 119; Gaps 21;

Db 244 DCSVENGGGEHNCNALPGARPCCPAGALQADGRSCSTASTQSCNDLCEHFCVNPDP--- 300
1244 ECKIMNGGCDTCTNSBGSTSCSBGYALMPDRSCA-----DIDE--CENNPDI CD 1294
Qy 301 -----QPSYSQCMCTGYRLADQHRCEVDVDCILBPSQCP-ORCVNTGGFECHCYPN 353
Db 1295 GGQCTNIPBEYRLCTGDFMAAMDMTKCIDVNECDLNSNICMPGECENTKGSFICHCQLG 1354
Qy 354 YDLVDGE--CVEVYDPC--FRANCEYOCPLN-OTSILCVCAEGEAPRPH-----EPRRC 403
Db 1355 YSVKKGTTGCTD--VDCECEIGHNCDMNASCLNIPGSFKSCSREGW--IGNGIKCIDLDEC 1411
Qy 404 QMFQNGTACPADDDPTQAS--CECEGYLLDGFICVDIDE-----CENG----- 447
Db 1412 SNGTHQCSINAQC-VNTPGSYRCACSEGP--TGDFFTSDVDECBENINLCENGQCLNTPG 1469
Qy 448 -----GF-----CSGVCHNLPTPEFICGPDALAHIG-- 476
Db 1470 AYRCBEMGFPTASDSRSCDIDECRFQNICVSGSTCNLPMFMHCICDDGYELDRTGNC 1529
Qy 477 TDCDSKGVDCDSDSGSEPPSP-----TPGSTLTPPAVLV----- 512
Db 1530 TDIDE-CADPINCNGLCVNTPGRYECNCPDPFLNPTGVCVDNRVGNCYLFGPRGDG 1588
Qy 513 ---HSGLLGISIASLCLVALLALCHLRKKG 543
Db 1589 SLSCNTEIGVGVSRSSC-----CSLGKAWG 1614

RESULT 11
A55184
fibulin-2 precursor - human
N:Alternate names: proteoin DXFZ586A1519.1
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C:Accession: A55184; T08744
C:Accession: A55184; T08744
Genomics 22, 425-430, 1994
A:Title: fibulin-2 (FBLN2): human cDNA sequence, mRNA expression, and mapping of the gene
A:Reference number: A55184; MIM:95104855; PMID:7806230
A:Accession: A55184
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1184 <ZHA>
A:Cross-references: UNIPROT:P98095; UNIPARC:UPI000012A567; GB:X82494; NID:9575232; PIDN:
R.Mamut, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, March 1999
A:Reference number: Z16471
A:Accession: T08744
A:Molecule type: mRNA

A:Residues: 656-719, 'QDECMGMDHDSRQPCVNTGSLFYCVNHTVLCADGYTLMAHRKCV', 720-853, 'T', 855-11
A:Cross-references: UNIPARC:UPI000006F3AD; EMBL:AL050095
A:Experimental source: adult uterus; clone DKFZp586A1519
C:Genetics:
A:Gene: GDB:FBLN2
A:Cross-references: GDB:293037; OMIM:135821
A:Map position: 3p25-3p24
A>Note: DKFZp586A1519.1
C:Superfamily: fibulin-2; EGF homology; von Willebrand factor type C repeat homology
C:Keywords: alternative splicing; extracellular matrix
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-1194/Product: fibulin-2 protein #status predicted <MAT>
F:905-941/Domain: EGF homology <EGF>

Query Match 11.3%; Score 363; DB 2; Length 1184;
Best Local Similarity 29.7%; Pred. No. 2,6e-14;
Matches 118; Conservative 29; Mismatches 124; Indels 126; Gaps 21;

QY 154 EEOQCEVAD-GFLCEHFHPATC-----RPLAV-----EPGMAAAVSTYGPFPARG 201
DB 531 EGQSCSNPNLGYPCN-HVMTSCGGEPLIVPEVRPRPEPAADRRVS-----EAM 582
QY 202 ADFQLPVGSSAAV---APLGLQMLCTAPRGAVQGHMABAGANDCSVENGCCHACNA 258
DB 583 AGREALSTGEHELPNLSLPGDDQDECLLPLBEL-----COHLCTIN 622
QY 259 IFGARPCCPAGALQADGRSC-----TAST-----QS 286
DB 623 TVGSHYACFPQFSLQDDGRKTRPRGHPQRPAPBPAKSRFQVAASTPLPLPQRYNT 682
QY 287 CND--LCHEFCVNPNDQPGSYSCMCETGYRLAADQRCEDVDCTLESPCP--QRVNT 342
DB 683 CKDNPCQKQVC---STVGSAALCSCEPGYAIWADVSCEDINECVTDLHTCSRGHCVNT 739
QY 343 QCGPECH---CYRYTVLDVDCVPEVVPCCFRANECYOCPLNQTSLYCV----- 388
DB 740 LGSFPCYALATCEPGLYALKDEG--BDVDEG--AMGTHTCQ---GFLCOMTKGSPYCOA 792
QY 389 ---CAEGFAPIPH-----BPHRCQMFNQTACPADCDPNTQASCEPBGY-I 431
DB 793 RQRCMDGLQDPBEGKCVINDICTSLSECRPEFSCLNTVGSTTCORNLPI---CARGYHA 849
QY 432 LDDGFTCTIDECENGFCGSG---VCHNLPGETFCIC 465
DB 850 SDDGAKCVDVNECETGVRHRCGEGQVCHLPGSYRDC 886

RESULT 12
T46488
Hypotheical protein DKFZp434J065.1 - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46488
R:Description: A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23035
A:Accession: T46488
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-741 <AAA>
A:Cross-references: UNIPROT:O8NDE6; UNIPARC:UPI000016ACCB; EMBL:AL137638
A:Experimental source: adult testis; clone DKFZp434J065
C:Genetics:
A>Note: DKFZp434J065.1

Query Match 11.2%; Score 358.5; DB 2; Length 741;
Best Local Similarity 31.6%; Pred. No. 3.2e-14;
Matches 86; Conservative 40; Mismatches 101; Indels 45; Gaps 15;

QY 245 CSVENGCCEHACNAIPGARPCCPAGALQADGRCTA--STQSCNDLCEHFCVNPQRP 302
DB 68 CAMEDHNCQQLCVNPGSFVQCYSGYALAEDEKRCVAVDYCASBNHCHEHCV--NAD-- 124

QY 303 GSYSCMCETGYRLAADQRCEDVDCTLESPBPQRCVNTGGEFCICPYNTDL-VDEGC 361
DB 125 GSYLCQCHGEGALNDEKTCIKTIDYCASBNHCQHECVNTDYSCHCLKGFLLNPDKT 184
QY 362 VEPDPRCF--RANCYQOQPLNQTSLYCVCAEGFAPIPH-----EPHCCQFIC 407
DB 185 CRRIYCALNPRGCEHCVNME--SYRCRHRGYTLDPNGKTCGRVDHCAQODHCEQLC 243
QY 408 NOTACPADCDPNTQAS--CEGEGYILDGF-ICTIDEC---ENGFCSGVCHNLPGTF 461
DB 244 -----LNTESFVQCSEGFILNEDLTKTSRVDYCLSDHG--CEYSCVMNDSF 291
QY 462 ECTGPDALARIHITGDCSGKVDG---GDG 490
DB 292 ACQC-PBGHVLRSQDKTC--AKLDSGALGDHG 320

RESULT 13
A49457

fibulin-2 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: A49457; S74095
R:Pan, T.C.; Sasaki, T.; Zhang, R.Z.; Paessler, R.; Timpl, R.; Chu, M.L.
J. Cell Biol. 123, 1269-1277, 1993
A:Title: Structure and expression of fibulin-2, a novel extracellular matrix protein wit
A:Reference number: A49457; MUID:94064787; PMID:8245130
A:Accession: A49457
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1221 <PAN>
A:Cross-references: UNIPROT:P37889; UNIPARC:UPI000029929; GB:X75285; NID:9437046; PIDN:
R:Sasaki, T.; Mann, K.; Murphy, G.; Chu, M.L.; Timpl, R.
Eur. J. Biochem. 240, 427-434, 1996
A:Title: Different susceptibilities of fibulin-1 and fibulin-2 to cleavage by matrix met
A:Reference number: S74094; MUID:96439073; PMID:8841408
A:Accession: S74095
A:Molecule type: protein
A:Residues: 236-238 'X', 240-247, 260-275, 336-344, 'L', 346-361, 405-426, 566-568, 'EW', 569-589
A:Cross-references: UNIPARC:UPI0000176509; UNIPARC:UPI000017650A; UNIPARC:UPI000017650B;
510; UNIPARC:UPI0000176511; UNIPARC:UPI0000176512
C:Superfamily: fibulin-2; EGF homology; von Willebrand factor type C repeat homology
C:Keywords: calcium binding; duplication; extracellular matrix; glycoprotein; homotrimer
F:942-978/Domain: EGF homology <EGF>

Query Match 11.1%; Score 356.5; DB 2; Length 1221;
Best Local Similarity 29.5%; Pred. No. 6.4e-14;
Matches 123; Conservative 39; Mismatches 140; Indels 115; Gaps 27;

QY 154 EEOQCEVAD-GFLCEHFHPATC-----RPLAV-----EPGMAAAVSTYGPFPARG 192
DB 521 EGQSCSNPNLGYPCN-HVMTSCGGEPLIVPEVRPRPEPAADRRVS-----EAM 579
QY 193 YGT---PFAARGADPQ---ALP-----VGSAAVAPLGLQML---CTAPPG 229
DB 580 LGTEBELPNLSLPGDDQDECLLPLBELQHLCTINTVGSGYRACFPGLQDGRICRPRDG 639
QY 230 AVQGHMABE-APGAMDSY-----ENGGECHACNAIPGARPCCPAGAA 272
DB 640 APQDTPARESAFRESAQSVPNTPLPVPQDNTCKDNGPCQVGRVAGDTAMCSGFPQYA 699
QY 273 LQADGRS-----CTASTQSCNDLCEHFCVNPQPGSYSC-----MCETGYRLAADQHR 321
DB 700 IMADGVSCEDDDECLMGTHDS--WKQPCV---NTLGSFYCVNHTVLCABGYILNA-HRK 753
QY 322 CEDVDCTLESPCP--PQRCVNTGGEFCCH---CYRYTVLDVDCVPEVVPDPCFRA--NC 373
DB 754 CVDINECVTDLHTCTRAHNCVNTPGSFQCYALATCEPGLYTLTDECTD--VDECVGTGTHNC 812
QY 374 E--YQOQPLNQTSLYCV---CAGFAPIPH-----BPHRCQMFNQTACPA 414
DB 813 QAGFSQCN-TKGSFYCOARQRCMDGFLQDPBEGKCVINDICTSLSECRPEFSCLNTVGSTY 871

Qy 415 DCDPNTQASCEPCPGY-ILDDGFICTDIDECENGSCFGSG---VCHNLPGTECTICGP 467
Db 872 TCQGNPLV---CGGHYANNEGSCVDVNECETGVHRCGEGQLCYNLPGSYRCCKP 925

RESULT 14

A38261
masking protein precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 09-Jul-2004
C:Accession: A38261
R:Tabu1, T.; Okada, F.; Yamaguchi, K.; Nakamura, T.
Proc. Natl. Acad. Sci. U.S.A. 87, 8835-8839, 1990
A:Title: Molecular cloning of the large subunit of transforming growth factor type beta
A:Reference number: A38261; MUID:91062373; PMID:2247454
A:Accession: A38261
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1712 <TSU>
A:Cross-references: UNIPROT:Q00918; UNIPARC:UPI000012B99B; GB:M55431; NID:9207285; PIDN:
F:911-947/Domain: EGF homology <EGF>

Query Match 10.4%; Score 333; DB 2; Length 1712;

Best Local Similarity 29.0%; Pred. No. 2,1e-12;

Matches 107; Conservative 44; Mismatches 130; Indels 88; Gaps 27;

Qy 177 PLAVEPGAAAVASTYGTTPFAAGADFOALPVGS---SAAVAPLGLQLM--CTAPPGA 230
Db 831 PUVVEKTSPPVPEVA-----PEGTSASQVIAPQVTEINECTVNDI 875
Qy 231 VQGHAREAPGAMDCSVENG-----GCEHA-----CNAIPGARPCQCP 268
Db 876 CGAGHCILPVRVYCTICEGVKFSQQRKCIDIDECQAQHLCSQRCENTEGSFLCICP 935
Qy 269 AGAALQADGRCTASTGSC--NDLC-EHFCVNPDPQPSYSC-METGYRLAADHRCED 324
Db 936 AGFLASEGSSNC-IDVDECLRPDYCRDRCI---NTAAAFRECYDGSRRMSRRGH-CE 990
Qy 325 VDDCILESPCP-ORCVNTQSGFEC-HCYPNYDLVDSGCVBPVDPCCFAN--CEYQCP 380
Db 991 IDECLTPSTCEBECVNSPGSYQCVPTCEGFRMNGQLD-VDECLQPKVCTNSCTNL 1048
Qy 381 NOTSYLCVCAEGFADIPHEPH-----RCQM--FCNQTACPADCDPNTQAS--CECPEGY 431
Db 1049 -EGSYMCSCHKYSPTPRHRQDIDECQGNLCNNGQC-----KNTDGSFRCTCGQGYQ 1102
Qy 432 L---DGFICTDIDECENGSCFSGVCHNLPGTECTICGPD---SALARHIG--TDC-- 479
Db 1103 LSAADQ---CEDIDECERHLCSHGQCRNTEGSPQLCNQGRASVLDGHCEDINECLE 1159
Qy 480 DSGKVDGD 488
Db 1160 DSSVCGGD 1168

RESULT 15

T43210
fibulin-1D precursor - Caenorhabditis elegans (fragment)

C:Species: Caenorhabditis elegans

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Apr-2004

C:Accession: T43210

R:Barth, J.L.; Argaves, K.M.; Roark, E.F.; Little, C.D.; Argaves, W.S.

submitted to the EMBL Data Library, June 1998

A:Description: Identification of chicken and C. elegans fibulin-1 homologs and character

A:Reference number: Z22337

A:Accession: T43210

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-589 <BAR>

A:Cross-references: UNIPARC:UPI000016B67E; EMBL:AF070477; PIDN:AAC24035.1

C:Genetics:
A>Note: intron positions not resolved (incomplete sequence)

Query Match 10.3%; Score 330.5; DB 2; Length 589;
Best Local Similarity 28.2%; Pred. No. 1.2e-12;
Matches 125; Conservative 49; Mismatches 172; Indels 97; Gaps 27;

Qy 103 GPLRGF-QWLTGDNNTSYRVARLDLNGAPLCGPLCAVSAAEATVSEPT-----WEEQ 156
Db 19 GCLRSFNKCGNDLEITH---ASEITGRPLNDPHVHLIDGRCASSHCHHCHDRGGEKV 75
Qy 157 QCEVKA-----DGLFCEFPF-ATCRPLAVE-----PGAAAAVSTYGTTPFA--- 198
Db 76 ECSRSRSGFDLAPDGMACVDHIDECATLMDCLIESQRCLNTPGSKRTLSGTYANDS 135
Qy 199 --AGADPQALPVSSSAAVAPLGLQMLCTAPGAVQ-----GHAREAPGAMDCS--- 246
Db 136 ETERCRDVEECNLSH---DCGPLYOCRTQSSRYCDACKKGGBLQNPNTGETSITTC 191
Qy 247 -----VENGCE-----HACNA-----IPGARPQCPAGAAALQADGRCTASTGSC 287
Db 192 PNGYTPKRMGNDIDECVTGHNCGAGECVNTPESPFCQKGN--LCAHYEVNAGATGFC 249
Qy 288 NDL--CEH-----FCVNPDPQPSYSCMETGYRLAADHRCEDVDDCLV---EPSPCP 336
Db 250 EDVNECQGVGSGMECI---NLPGTYKCKGSPGYEFNDAKKRCHDVDECIKFAGVCDLS 306
Qy 337 ORCVNTQSGFECCHCYPNYDLV-DGCVBPVDPCCR--ANCEYQCPPLNQTSYLCAEGF 393
Db 307 AECTNITGSPFECKKPGFOLASDGRCEVDNVECTGTIAACQKCVNI-PSYQCTCDRGF 365
Qy 394 APIP-----HEPRHCOMFC--NOTACPADCDPNTQAS--CECPEGY-ILDDGFICTDIDE 443
Db 366 ALGPDGTCEIDIDECSTWAGSGNDLCMGGC--INTKGSYLQCPFGYKIQPGRCTVDVDE 424
Qy 444 CENGSGFCG---VCHNLPGTEFC 463
Db 425 CAMGE-CAGSDKVCVNTLGSFKC 446

Search completed: February 4, 2006, 04:32:59
Job time : 47 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

This book (1930)
(1930) 1930

GenCore version 5.1.7
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OM protein - protein search, using BW model

Run on: February 4, 2006, 04:32:27 ; Search time 51 Seconds
(without alignments)
930.507 Million cell updates/sec

Title: US-10-725-013-2

Perfect score: 3203
Sequence: 1 MGVLTGALALAGLGPAP.....APSKVVIQVHRTTPTQL 574

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
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3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PTCTUS_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	3176.5	99.2	575	1 US-08-312-870-1	Sequence 1, Appli
2	3176.5	99.2	575	2 US-09-949-002-296	Sequence 296, App
3	3176.5	99.2	575	6 5466668-6	Patent No. 5466668
4	3176.5	99.2	682	2 US-09-949-002-436	Sequence 436, App
5	3172.5	99.0	575	1 US-08-261-206A-59	Sequence 59, Appli
6	3172.5	99.0	575	2 US-09-880-484D-2	Sequence 2, Appli
7	3172.5	99.0	575	2 US-10-438-648-2	Sequence 2, Appli
8	3168.5	98.9	575	1 US-08-170-290A-54	Sequence 54, Appli
9	3107	97.0	572	6 5256770-7	Patent No. 5256770
10	2885.5	90.1	516	2 US-09-509-994-2	Sequence 2, Appli
11	2881.5	90.0	516	2 US-09-509-994-1	Sequence 1, Appli
12	2795.5	87.3	458	1 US-08-733-564-2	Sequence 2, Appli
13	2793.5	87.2	497	1 US-08-312-870-3	Sequence 3, Appli
14	2789.5	87.1	497	2 US-09-331-793-4	Sequence 4, Appli
15	2735.5	85.4	494	1 US-08-014-723-14	Sequence 14, Appli
16	2733.5	85.4	494	1 US-08-110-011A-14	Sequence 14, Appli
17	2733.5	85.3	494	1 US-08-014-723-16	Sequence 16, Appli
18	2733.5	85.3	494	1 US-08-110-011A-16	Sequence 16, Appli
19	2659.5	83.0	475	1 US-08-307-444A-2	Sequence 2, Appli
20	2659.5	83.0	475	1 US-08-587-389-2	Sequence 2, Appli
21	2655.5	82.9	475	1 US-08-307-444A-1	Sequence 1, Appli
22	2655.5	82.9	475	1 US-08-587-389-1	Sequence 1, Appli
23	2649.5	82.7	476	1 US-08-014-723-1	Sequence 1, Appli
24	2649.5	82.7	476	1 US-08-110-011A-1	Sequence 1, Appli
25	2647.5	82.7	476	1 US-08-014-723-2	Sequence 2, Appli
26	2647.5	82.7	476	1 US-08-014-723-18	Sequence 18, Appli
27	2647.5	82.7	476	1 US-08-110-011A-2	Sequence 2, Appli

28	2647.5	82.7	476	1 US-08-110-011A-18	Sequence 18, Appli
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34	2512.5	78.4	446	1 US-08-587-389-5	Sequence 5, Appli
35	1590.5	49.7	275	1 US-08-312-870-5	Sequence 5, Appli
36	1323	41.3	239	2 US-10-104-047-2759	Sequence 2759, Ap
37	1159	36.2	215	1 US-08-312-870-9	Sequence 9, Appli
38	689	21.5	115	1 US-08-733-564-1	Sequence 1, Appli
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40	587.5	18.3	652	1 US-09-949-016-6963	Sequence 6963, Ap
41	578	18.0	757	2 US-09-949-016-8087	Sequence 8087, Ap
42	578	18.0	758	2 US-09-724-864-39	Sequence 39, Appli
43	573	17.9	492	2 US-09-949-092-10403	Sequence 10403, A
44	384	12.0	1935	2 US-09-538-092-1076	Sequence 1076, Ap
45	384	12.0	2871	2	

ALIGNMENTS

RESULT 1
US-08-312-870-1
Sequence 1, Application US/08312870
Patent No. 5639625
GENERAL INFORMATION:
APPLICANT: Carson, Craig W.
TITLE OF INVENTION: Method for Detecting Antibodies to
TITLE OF INVENTION: Thrombomodulin in Patients
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,870
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMRF B35150
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4600
FAX: 214-939-4600
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: Protein
LOCATION: 19..575
US-08-312-870-1
Query Match 99.2%; Score 3176.5; DB 1; Length 575;
Best local similarity 99.5%; Pred. No. 4.5e-221;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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OY 1 MGVLVLTGALALAGLGFPAAPAPBPQSGSCVEHDCFALYPGPATPLNASQICDGLRGHLM 60
DB 1 MLGVLVLTGALALAGLGFPAAPAPBPQSGSCVEHDCFALYPGPATPLNASQICDGLRGHLM 60
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DB 61 TVRSSVAADVLSLLINGDGVGRRRLMTGLQLPFCGCPKRLGPIRGQWVTGDNNTSYS 120
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DB 241 GAMDCSVENGCCEHACNAIPGARPCQCPAGALQADGSCCTASATQSCNDLCEHFCVNP 299
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DB 300 DQPGSYSCMCTGYRLADQHRCEVDVDCILEBSPCPCRVNTQGGFCHCYPNYDLVDG 359
OY 360 ECVEPVDCFPANACEYCCQPLNQTSYLCVCAEGFAPIDHEPHRCMFCNQACPADCDPN 419
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DB 540 KKGGAARAKMEYKCAAPSKAVLVLOHVTERTPQRL 574
OY 541 KKGGAARAKMEYKCAAPSKAVLVLOHVTERTPQRL 575
DB 541 KKGGAARAKMEYKCAAPSKAVLVLOHVTERTPQRL 575
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RESULT 2
US-09-949-002-296
; Sequence 296, Application US/09949002
; Patent No. 5900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: C1000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-296
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Query Match 99.2%; Score 3176.5; DB 2; Length 575;
Best Local Similarity 99.5%; Pred. No. 4.5e-221;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
OY 1 MGVLVLTGALALAGLGFPAAPAPBPQSGSCVEHDCFALYPGPATPLNASQICDGLRGHLM 60
DB 1 MLGVLVLTGALALAGLGFPAAPAPBPQSGSCVEHDCFALYPGPATPLNASQICDGLRGHLM 60
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DB 181 EPGAAAALVSTTGTTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPGAVQGHAREAP 240
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RESULT 3
5466668-6
; Patent No. 5466668
; APPLICANT: GLASER, CHARLES B.; MORSE, MICHAEL J.; LIGHT,
; DAVID R.
; TITLE OF INVENTION: SUPERIOR THROMBOMODULIN ANALOGS FOR
; PHARMACEUTICAL USE
; NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,346
; FILING DATE: 22-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 568,456
; FILING DATE: 15-AUG-1990
; APPLICATION NUMBER: 506,325
; FILING DATE: 09-APR-1990
; APPLICATION NUMBER: 406,941
; FILING DATE: 13-SEP-1989
; APPLICATION NUMBER: 345,374
; FILING DATE: 28-APR-1989
; SEQ ID NO:6;
; LENGTH: 575
5466668-6
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Query Match 99.2%; Score 3176.5; DB 6; Length 575;
Best Local Similarity 99.5%; Pred. No. 4.5e-221;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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DB 1 MLGVLVLTGALALAGLGFPAAPAPBPQSGSCVEHDCFALYPGPATPLNASQICDGLRGHLM 60
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DB 61 TVRSSVAADVLSLLINGDGVGRRRLMTGLQLPFCGCPKRLGPIRGQWVTGDNNTSYS 120
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DB 121 RWARLDLNGAPLCGFLCVAVSAEAATVPSBPWEQOCVEKADGFLCEFHFPATCRPLAV 180
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RESULT 4

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US-09-949-002-436
; Sequence 436, Application US/09949002
; Patent No. 6200016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: C1000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 436
; LENGTH: 682
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-436
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Query Match 99.2%; Score 3176.5; DB 2; Length 682;
Best Local Similarity 99.5%; Pred. No. 5-5e-221;
Matches 572; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Db 108 MLGVIVLICALALAGIAPPAAPAPQPGSGQCVENHDFALYPGPATPLNASQICDGLRGHLM 167
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Db 228 RMARLDLNGAPLCPGLCVAVSNAAEATVSEPTWEEQGCCKADGFLCEHFPAATCRPLAV 287
Qy 181 EBGAAAAAASITVGTTPFAARGADFOALPVGSSAAVAFLGLQIMCTAPPGAVOGHWAREAP 240
Db 288 EBGAAAAAASITVGTTPFAARGADFOALPVGSSAAVAFLGLQIMCTAPPGAVOGHWAREAP 347
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Qy 241 GAMDCSVENGGEHCNAINIPGARPCQCPAGALQADGSCITAS-TQSCNDLCEHFCVNP 299
Db 348 GAMDCSVENGGEHCNAINIPGARPCQCPAGALQADGSCITASATQSCNDLCEHFCVNP 407
Qy 300 DQPGSYSCMCEGTGYLAADQHRCEVDVDCILBSPCPCVCNTQGGFECHCPANVDVNG 359
Db 408 DQPGSYSCMCEGTGYLAADQHRCEVDVDCILBSPCPCVCNTQGGFECHCPANVDVNG 467
Qy 360 ECEVEVDPCFRANCEYOCOPLNQTSYLCVCAEGFAPIPHEPRCOMFCNQTCAPADCDPN 419
Db 468 ECEVEVDPCFRANCEYOCOPLNQTSYLCVCAEGFAPIPHEPRCOMFCNQTCAPADCDPN 527
Qy 420 TQASCECEBGYLDDGFICTDIDECENGFGSCGVCHNLPGTFECICGPDALARIHIGTDC 479
Db 528 TQASCECEBGYLDDGFICTDIDECENGFGSCGVCHNLPGTFECICGPDALARIHIGTDC 587
Qy 480 DSGKVDGDSGSGEPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
Db 588 DSGKVDGDSGSGEPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 647
Qy 540 KKGGAARAMEYKCAAPSKEVVLQHVTRTERTPORL 574
Db 648 KKGGAARAMEYKCAAPSKEVVLQHVTRTERTPORL 682
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RESULT 5

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US-08-261-206A-59
; Sequence 59, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
; WITH THROMBIN
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,206A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,492
; FILING DATE: 03-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 216-275P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEFAX: 248345
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 575 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Protein
LOCATION: 1..575
OTHER INFORMATION: /label= protein
OTHER INFORMATION: /note= "human thrombomodulin"
US-08-261-206A-59
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Query Match          99.0%; Score 3172.5; DB 1; Length 575;
Best Local Similarity 99.3%; Pred. No. 8.8e-221;
Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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QY 1 MLGVLVIGALALAGLGPAPAEPPQGSQCVEHDCFPALYPGPATFLNLSQICDGLRGHLM 60
DB 1 MLGVLVIGALALAGLGPAPAEPPQGSQCVEHDCFPALYPGPATFLNLSQICDGLRGHLM 60
QY 61 TVRSSVADVLSLLNGDGVGRRRLMTGLQLPFGCGDPKRLGRLRGOWTGDNNNTSYS 120
DB 61 TVRSSVADVLSLLNGDGVGRRRLMTGLQLPFGCGDPKRLGRLRGOWTGDNNNTSYS 120
QY 121 RMARLDLNGAPLCEPLCVAVSAEAATVPSSEPIWEEQCEVADGFLCEFHFPATCRPLAV 180
DB 121 RMARLDLNGAPLCEPLCVAVSAEAATVPSSEPIWEEQCEVADGFLCEFHFPATCRPLAV 180
QY 181 EPGAALAAVSTTYGTPFAARGADFOALPVSSAAVAAPLGLQIMCTAPPGAVQGHMAREAP 240
DB 181 EPGAALAAVSTTYGTPFAARGADFOALPVSSAAVAAPLGLQIMCTAPPGAVQGHMAREAP 240
QY 241 GAMDCSVENGGCEHCNNAIPGARPCQCPAGALQADGSCCTAS-TQSCNDLCEHFCVNP 299
DB 241 GAMDCSVENGGCEHCNNAIPGARPCQCPAGALQADGSCCTAS-TQSCNDLCEHFCVNP 299
QY 300 DQPGSYSCMCTGYRLAADQHRCEVDVDCILEPSPCPCRVNTQGGFECCHCPYNYDLVDG 359
DB 300 DQPGSYSCMCTGYRLAADQHRCEVDVDCILEPSPCPCRVNTQGGFECCHCPYNYDLVDG 359
QY 361 ECVEVPDPCFRANCEYQCOPLNQTYSYLCVCAEGFAPIPHEPRCOMFCNQACPADCDPN 419
DB 361 ECVEVPDPCFRANCEYQCOPLNQTYSYLCVCAEGFAPIPHEPRCOMFCNQACPADCDPN 419
QY 420 TQASCECEGYILDDGFLCTDIDECENGFGSGVCHNLPGTRECICGPDLSALVRIHIGTDC 479
DB 420 TQASCECEGYILDDGFLCTDIDECENGFGSGVCHNLPGTRECICGPDLSALVRIHIGTDC 479
QY 480 DSGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALCHLR 539
DB 480 DSGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALCHLR 539
QY 540 KKGGAARAMEYKCAAPSEKVVLLQHVTERTERPQRL 574
DB 540 KKGGAARAMEYKCAAPSEKVVLLQHVTERTERPQRL 574
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RESULT 6
US-09-880-484D-2
; Sequence 2, Application US/09880484D
; Patent No. 6632791
; GENERAL INFORMATION:
; APPLICANT: Light, David
; APPLICANT: Nagashima, Mariko
; APPLICANT: Morser, Michael J
; TITLE OF INVENTION: Thrombomodulin Analogs for Pharmaceutical Use
; FILE REFERENCE: 51863AUSM1
; CURRENT APPLICATION NUMBER: US/09/880,484D
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/213,678
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 575
; TYPE: PRT
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ORGANISM: Homo sapiens
US-09-880-484D-2
Query Match          99.0%; Score 3172.5; DB 2; Length 575;
Best Local Similarity 99.3%; Pred. No. 8.8e-221;
Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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QY 1 MLGVLVIGALALAGLGPAPAEPPQGSQCVEHDCFPALYPGPATFLNLSQICDGLRGHLM 60
DB 1 MLGVLVIGALALAGLGPAPAEPPQGSQCVEHDCFPALYPGPATFLNLSQICDGLRGHLM 60
QY 61 TVRSSVADVLSLLNGDGVGRRRLMTGLQLPFGCGDPKRLGRLRGOWTGDNNNTSYS 120
DB 61 TVRSSVADVLSLLNGDGVGRRRLMTGLQLPFGCGDPKRLGRLRGOWTGDNNNTSYS 120
QY 121 RMARLDLNGAPLCEPLCVAVSAEAATVPSSEPIWEEQCEVADGFLCEFHFPATCRPLAV 180
DB 121 RMARLDLNGAPLCEPLCVAVSAEAATVPSSEPIWEEQCEVADGFLCEFHFPATCRPLAV 180
QY 181 EPGAALAAVSTTYGTPFAARGADFOALPVSSAAVAAPLGLQIMCTAPPGAVQGHMAREAP 240
DB 181 EPGAALAAVSTTYGTPFAARGADFOALPVSSAAVAAPLGLQIMCTAPPGAVQGHMAREAP 240
QY 241 GAMDCSVENGGCEHCNNAIPGARPCQCPAGALQADGSCCTAS-TQSCNDLCEHFCVNP 299
DB 241 GAMDCSVENGGCEHCNNAIPGARPCQCPAGALQADGSCCTAS-TQSCNDLCEHFCVNP 299
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DB 300 DQPGSYSCMCTGYRLAADQHRCEVDVDCILEPSPCPCRVNTQGGFECCHCPYNYDLVDG 359
QY 361 ECVEVPDPCFRANCEYQCOPLNQTYSYLCVCAEGFAPIPHEPRCOMFCNQACPADCDPN 419
DB 361 ECVEVPDPCFRANCEYQCOPLNQTYSYLCVCAEGFAPIPHEPRCOMFCNQACPADCDPN 419
QY 420 TQASCECEGYILDDGFLCTDIDECENGFGSGVCHNLPGTRECICGPDLSALVRIHIGTDC 479
DB 420 TQASCECEGYILDDGFLCTDIDECENGFGSGVCHNLPGTRECICGPDLSALVRIHIGTDC 479
QY 480 DSGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALCHLR 539
DB 480 DSGKVDGSDSGSGEPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALCHLR 539
QY 540 KKGGAARAMEYKCAAPSEKVVLLQHVTERTERPQRL 574
DB 540 KKGGAARAMEYKCAAPSEKVVLLQHVTERTERPQRL 574
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RESULT 7
US-10-438-648-2
; Sequence 2, Application US/10438648
; Patent No. 6790828
; GENERAL INFORMATION:
; APPLICANT: Light, David
; APPLICANT: Nagashima, Mariko
; APPLICANT: Morser, Michael J
; TITLE OF INVENTION: Thrombomodulin Analogs for Pharmaceutical Use
; FILE REFERENCE: 51863AUSD1
; CURRENT APPLICATION NUMBER: US/10/438,648
; PRIOR FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US 60/213,678
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 09/880,484
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-438-648-2
Query Match          99.0%; Score 3172.5; DB 2; Length 575;
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Best Local Similarity 99.3%; Pred. No. 8.8e-221;
Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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OY 1 MLGVLVIGALALAGLPAPAPAPPOGSGQCVHEHDCFALYPGPATFLNASQICDGLRGHLM 60
DB 1 MLGVLVIGALALAGLPAPAPAPPOGSGQCVHEHDCFALYPGPATFLNASQICDGLRGHLM 60
OY 61 TRSSVADVISLILNDGGVGRRLWIGLQIPGCGDPKRLGRLRGFWYTGDNNTSYS 120
DB 61 TRSSVADVISLILNDGGVGRRLWIGLQIPGCGDPKRLGRLRGFWYTGDNNTSYS 120
OY 121 RMARLDLNGAPLCGPLCAVNSAATVPSSEPIWEEQCEVADGFLCEFHFPATCRPLAV 180
DB 121 RMARLDLNGAPLCGPLCAVNSAATVPSSEPIWEEQCEVADGFLCEFHFPATCRPLAV 180
OY 181 EPGAAAAVSTTYGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHWAREAP 240
DB 181 EPGAAAAVSTTYGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHWAREAP 240
OY 241 GAMDCSVENGGCEHACNAIPGAPPCQCPAGALQADGRSCTAS-TQSCNDLCEHFCVNP 299
DB 241 GAMDCSVENGGCEHACNAIPGAPPCQCPAGALQADGRSCTASATQSCNDLCEHFCVNP 300
OY 300 DQPSYSQCEGTGRLAADQRCEDVDCCIIEPSPCQRCVNTQSGFECCHCYPNYDLVDG 359
DB 301 DQPSYSQCEGTGRLAADQRCEDVDCCIIEPSPCQRCVNTQSGFECCHCYPNYDLVDG 360
OY 360 ECVBPVPCFRANCEYOCQPLNOTSYLCVCAEGFAPIPHEBPRCOMFCNOTACPADCPN 419
DB 361 ECVBPVPCFRANCEYOCQPLNOTSYLCVCAEGFAPIPHEBPRCOMFCNOTACPADCPN 420
OY 420 TQASCCEPEGYILDDGFICTDIDECENGFCGVCCHNLPGTFECICGPDLSALAHIGTDC 479
DB 421 TQASCCEPEGYILDDGFICTDIDECENGFCGVCCHNLPGTFECICGPDLSALAHIGTDC 480
OY 480 DSGKVDGDSGSGPPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
DB 481 DSGKVDGDSGSGPPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540
OY 540 KKGAAARAKMEYKCAAPSKVVLQHVTERTPORL 574
DB 541 KKGAAARAKMEYKCAAPSKVVLQHVTERTPORL 575
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RESULT 8

US-08-170-290A-54
Sequence 54, Application US/08170290A
Patent No. 5702931
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Morse, Michael J.
APPLICANT: Ziehlender, Laura R.
TITLE OF INVENTION: No. 5702931el Mitogenesis Methods and
TITLE OF INVENTION: Compositions
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSEE: James M. Heslin
STREET: 379 Lytton Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-170,290A
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05573

FILING DATE: 01-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/724,237
FILING DATE: 01-JUL-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 11972-58-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
FAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-170-290A-54

Query Match 98.9%; Score 3168.5; DB 1; Length 575;
Best Local Similarity 99.3%; Pred. No. 1.7e-220;
Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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OY 1 MLGVLVIGALALAGLPAPAPAPPOGSGQCVHEHDCFALYPGPATFLNASQICDGLRGHLM 60
DB 1 MLGVLVIGALALAGLPAPAPAPPOGSGQCVHEHDCFALYPGPATFLNASQICDGLRGHLM 60
OY 61 TRSSVADVISLILNDGGVGRRLWIGLQIPGCGDPKRLGRLRGFWYTGDNNTSYS 120
DB 61 TRSSVADVISLILNDGGVGRRLWIGLQIPGCGDPKRLGRLRGFWYTGDNNTSYS 120
OY 121 RMARLDLNGAPLCGPLCAVNSAATVPSSEPIWEEQCEVADGFLCEFHFPATCRPLAV 180
DB 121 RMARLDLNGAPLCGPLCAVNSAATVPSSEPIWEEQCEVADGFLCEFHFPATCRPLAV 180
OY 181 EPGAAAAVSTTYGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHWAREAP 240
DB 181 EPGAAAAVSTTYGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHWAREAP 240
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DB 241 GAMDCSVENGGCEHACNAIPGAPPCQCPAGALQADGRSCTASATQSCNDLCEHFCVNP 300
OY 300 DQPSYSQCEGTGRLAADQRCEDVDCCIIEPSPCQRCVNTQSGFECCHCYPNYDLVDG 359
DB 301 DQPSYSQCEGTGRLAADQRCEDVDCCIIEPSPCQRCVNTQSGFECCHCYPNYDLVDG 360
OY 360 ECVBPVPCFRANCEYOCQPLNOTSYLCVCAEGFAPIPHEBPRCOMFCNOTACPADCPN 419
DB 361 ECVBPVPCFRANCEYOCQPLNOTSYLCVCAEGFAPIPHEBPRCOMFCNOTACPADCPN 420
OY 420 TQASCCEPEGYILDDGFICTDIDECENGFCGVCCHNLPGTFECICGPDLSALAHIGTDC 479
DB 421 TQASCCEPEGYILDDGFICTDIDECENGFCGVCCHNLPGTFECICGPDLSALAHIGTDC 480
OY 480 DSGKVDGDSGSGPPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
DB 481 DSGKVDGDSGSGPPSPPTGSLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 540
OY 540 KKGAAARAKMEYKCAAPSKVVLQHVTERTPORL 574
DB 541 KKGAAARAKMEYKCAAPSKVVLQHVTERTPORL 575
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RESULT 9

US-08-170-290A-54
Sequence 54, Application US/08170290A
Patent No. 5256770
GENERAL INFORMATION:
APPLICANT: GLASER, CHARLES B.; MORSE, MICHAEL J.; LIGHT,
DAVID R.
TITLE OF INVENTION: OXIDATION RESISTANT THROMBOMODULIN ANALOGS
NUMBER OF SEQUENCES: 48

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/506,325
; FILING DATE: 09-APR-1990
; SEQ ID NO: 7
; LENGTH: 572
5256770-7
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Query Match          97.0%; Score 3107; DB 6; Length 572;
Best Local Similarity 98.3%; Pred. No. 4,6e-216;
Matches 565; Conservative 0; Mismatches 6; Indels 4; Gaps 3;
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DB 61 TVRSSVADVLSLLNDGGVGRRLMTGLQLPGCGDPRKLGRLGFGQWVTGDNNTSYS 119
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QY 241 GAMDCSVENGGCEHCNAINPGAPRCQCPAGALQADGSCITAS--TOSGNDLCEHFCVNP 299
DB 238 GAMDCSVENGGCEHCNAINPGAPRCQCPAGALQADGSCITASOSGNDLCEHFCVNP 297
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DB 358 ECEVBPDCFRANCEYOCQPLNQTSYLCVCAEGFAPPIHEBRCQMFNCQTCAPADCPN 417
QY 420 TQASCECEGYILDDGFICTDIDECENGFCGVCCHNLPGTFECICGSDSALARIIGTDC 479
DB 418 TQASCECEGYILDDGFICTDIDECENGFCGVCCHNLPGTFECICGSDSALARIIGTDC 477
QY 480 DSGKVDGDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 539
DB 478 DSGKVDGDSGSGEPSPPTPGSTLTPPAVGLVHSGLLIGISIASLCLVALLALLCHLR 537
QY 540 KKGGAARAKMEYKCAAPSEKVVLLQHVRTERTPORL 574
DB 538 KKGGAARAKMEYKCAAPSEKVVLLQHVRTERTPORL 572

RESULT 10
US-09-509-994-2
; Sequence 2, Application US/09509994
; Patent No. 6808706
; GENERAL INFORMATION:
; APPLICANT: YUI, MASAKI
; APPLICANT: YOKOZAWA, AKIRA
; APPLICANT: MURATA, TOMOYO
; APPLICANT: TSURUTA, KAZUHISA
; APPLICANT: SHIMIZU, HIROKOTO
; TITLE OF INVENTION: METHOD FOR KEEPING THE QUALITY OF AQUEOUS PARENTERAL
; TITLE OF INVENTION: SOLUTION OF THROMBOMODULIN IN STORAGE AND DISTRIBUTION
; FILE REFERENCE: KP-8753
; CURRENT APPLICATION NUMBER: US/09/509,994
; CURRENT FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: PCT/JP98/04609
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: JP 9-281659
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: JP 9-308523
; PRIOR FILING DATE: 1997-11-11
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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentm Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Partial amino acid sequences of a human
; OTHER INFORMATION: Thrombomodulin
US-09-509-994-2
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Query Match          90.1%; Score 2885.5; DB 2; Length 516;
Best Local Similarity 99.4%; Pred. No. 3,8e-200;
Matches 513; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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QY 1 MLGVLVIGALALAGLGPAPAPAPPGSGQCYEHDCFLALYPGPATFLNASQICDGLRGLM 60
DB 1 MLGVLVIGALALAGLGPAPAPAPPGSGQCYEHDCFLALYPGPATFLNASQICDGLRGLM 60
QY 61 TVRSSVADVLSLLNDGGVGRRLMTGLQLPGCGDPRKLGRLGFGQWVTGDNNTSYS 120
DB 61 TVRSSVADVLSLLNDGGVGRRLMTGLQLPGCGDPRKLGRLGFGQWVTGDNNTSYS 120
QY 121 RMARLDLNGAPLCPGLCVAVSAEAATVPSEPIWEEOCEVADGFLCEFHFPATCRPLAV 180
DB 121 RMARLDLNGAPLCPGLCVAVSAEAATVPSEPIWEEOCEVADGFLCEFHFPATCRPLAV 180
QY 181 EPGAAAAVSTITGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPAVQGHMAREAP 240
DB 181 EPGAAAAVSTITGTPFAARGADFOALPVGSSAAVAPLGLQIMCTAPPAVQGHMAREAP 240
QY 241 GAMDCSVENGGCEHCNAINPGAPRCQCPAGALQADGSCITAS--TOSGNDLCEHFCVNP 299
DB 241 GAMDCSVENGGCEHCNAINPGAPRCQCPAGALQADGSCITASOSGNDLCEHFCVNP 299
QY 300 DQPSYSCMCEGTGRILADQRCEDVDCCIIEPSPCPORCVNTGGFECCHCPYNDLVDG 359
DB 301 DQPSYSCMCEGTGRILADQRCEDVDCCIIEPSPCPORCVNTGGFECCHCPYNDLVDG 360
QY 360 ECEVBPDCFRANCEYOCQPLNQTSYLCVCAEGFAPPIHEBRCQMFNCQTCAPADCPN 419
DB 361 ECEVBPDCFRANCEYOCQPLNQTSYLCVCAEGFAPPIHEBRCQMFNCQTCAPADCPN 420
QY 420 TQASCECEGYILDDGFICTDIDECENGFCGVCCHNLPGTFECICGSDSALARIIGTDC 479
DB 421 TQASCECEGYILDDGFICTDIDECENGFCGVCCHNLPGTFECICGSDSALARIIGTDC 480
QY 480 DSGKVDGDSGSGEPSPPTPGSTLTPPAVGLVHSG 515
DB 481 DSGKVDGDSGSGEPSPPTPGSTLTPPAVGLVHSG 516
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RESULT 11
US-09-509-994-1
; Sequence 1, Application US/09509994
; Patent No. 6808706
; GENERAL INFORMATION:
; APPLICANT: YUI, MASAKI
; APPLICANT: YOKOZAWA, AKIRA
; APPLICANT: MURATA, TOMOYO
; APPLICANT: TSURUTA, KAZUHISA
; APPLICANT: SHIMIZU, HIROKOTO
; TITLE OF INVENTION: METHOD FOR KEEPING THE QUALITY OF AQUEOUS PARENTERAL
; TITLE OF INVENTION: SOLUTION OF THROMBOMODULIN IN STORAGE AND DISTRIBUTION
; FILE REFERENCE: KP-8753
; CURRENT APPLICATION NUMBER: US/09/509,994
; CURRENT FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: PCT/JP98/04609
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: JP 9-281659
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: JP 9-308523
; PRIOR FILING DATE: 1997-11-11
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 516
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
OTHER INFORMATION: Partial amino acid sequences of a human
US-09-509-994-1

Query Match 90.0%; Score 2881.5; DB 2; Length 516;
Best Local Similarity 99.2%; Pred. No. 7.4e-200;
Matches 512; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MLGVLVIGALALAGLGPAPAPBPQGSQCVHDCFLYPGPATFLNASQICDGLRGLM 60
DB 1 MLGVLVIGALALAGLGPAPAPBPQGSQCVHDCFLYPGPATFLNASQICDGLRGLM 60
QY 61 TRSSVADVISLILNGDGVGRRLWIGLQLPGCCGDKRLGPRGFQWVTGDNNTSYS 120
DB 61 TRSSVADVISLILNGDGVGRRLWIGLQLPGCCGDKRLGPRGFQWVTGDNNTSYS 120
QY 121 RWARLDLNGAPLCPGLCVAVSAEAATVSEPIWEQCEVADGFLCEFHFPATCRPLAV 180
DB 121 RWARLDLNGAPLCPGLCVAVSAEAATVSEPIWEQCEVADGFLCEFHFPATCRPLAV 180
QY 181 EPGAAAAVSTTGTGPPARAGADPOLPVGSSAAVAPLGLQIMCTAPGAVQGHARAP 240
DB 181 EPGAAAAVSTTGTGPPARAGADPOLPVGSSAAVAPLGLQIMCTAPGAVQGHARAP 240
QY 241 GAMPSCVENGCCEHACNAIPGARPCQCPAGALQADGSCITAS-TQSCNDLCEHFCVNP 299
DB 241 GAMPSCVENGCCEHACNAIPGARPCQCPAGALQADGSCITAS-TQSCNDLCEHFCVNP 299
QY 300 DQPSYSCMCTGYRLADQRCBDDVDCILPSPCPQRCVNTQGFECCHCYPNYDLVDG 359
DB 300 DQPSYSCMCTGYRLADQRCBDDVDCILPSPCPQRCVNTQGFECCHCYPNYDLVDG 359
QY 360 ECVRPVPCFRANCBYOCQPLNQTSTYLCVCAEGFAPRPHBPHRCMPCNQTCAPADCBPN 419
DB 360 ECVRPVPCFRANCBYOCQPLNQTSTYLCVCAEGFAPRPHBPHRCMPCNQTCAPADCBPN 419
QY 420 TQACECEGEGYILDDGFICTIDECENGFGSGVCHNLPGTFECICGPDALARIHIGTDC 479
DB 420 TQACECEGEGYILDDGFICTIDECENGFGSGVCHNLPGTFECICGPDALARIHIGTDC 479
QY 480 DSGKVDGDSGSGEPPSPPTGSLTPPAVGLVHSG 515
DB 480 DSGKVDGDSGSGEPPSPPTGSLTPPAVGLVHSG 515

RESULT 12
US-08-733-564-2
Sequence 2, Application US/08733564
Patent No. 5916874
GENERAL INFORMATION:
APPLICANT: FUJIMURA, Kenji
APPLICANT: MOCHIDA, Satoshi
TITLE OF INVENTION: METHOD FOR TREATING LIVER INJURY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolaesch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/733,564
FILING DATE: 18 OCTOBER 1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 0216-0362P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-733-564-2

Query Match 87.3%; Score 2795.5; DB 1; Length 498;
Best Local Similarity 99.2%; Pred. No. 1.1e-193;
Matches 494; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 19 AAPBPQGSQCVHDCFLYPGPATFLNASQICDGLRGLMTVRSSVADVISLILNGD 78
DB 1 AAPBPQGSQCVHDCFLYPGPATFLNASQICDGLRGLMTVRSSVADVISLILNGD 78
QY 79 GGVGRRLWIGLQLPGCCGDKRLGPRGFQWVTGDNNTSYSRWARLDLNGAPLCPGLCV 138
DB 79 GGVGRRLWIGLQLPGCCGDKRLGPRGFQWVTGDNNTSYSRWARLDLNGAPLCPGLCV 138
QY 139 AVSAEAATVSEPIWEQCEVADGFLCEFHFPATCRPLAVEGAAAAVSTTGTGPPA 198
DB 139 AVSAEAATVSEPIWEQCEVADGFLCEFHFPATCRPLAVEGAAAAVSTTGTGPPA 198
QY 121 AVSAEAATVSEPIWEQCEVADGFLCEFHFPATCRPLAVEGAAAAVSTTGTGPPA 180
DB 121 AVSAEAATVSEPIWEQCEVADGFLCEFHFPATCRPLAVEGAAAAVSTTGTGPPA 180
QY 199 ARGADPOLPVGSSAAVAPLGLQIMCTAPGAVQGHARAPGAMDCSVENGCCEHACNA 258
DB 199 ARGADPOLPVGSSAAVAPLGLQIMCTAPGAVQGHARAPGAMDCSVENGCCEHACNA 258
QY 181 ARGADPOLPVGSSAAVAPLGLQIMCTAPGAVQGHARAPGAMDCSVENGCCEHACNA 240
DB 181 ARGADPOLPVGSSAAVAPLGLQIMCTAPGAVQGHARAPGAMDCSVENGCCEHACNA 240
QY 259 IPGARPCQCPAGALQADGSCITAS-TQSCNDLCEHFCVNPDPGYSCECEGYRLAA 317
DB 259 IPGARPCQCPAGALQADGSCITAS-TQSCNDLCEHFCVNPDPGYSCECEGYRLAA 317
QY 241 IPGARPCQCPAGALQADGSCITASATQSCNDLCEHFCVNPDPGYSCECEGYRLAA 300
DB 241 IPGARPCQCPAGALQADGSCITASATQSCNDLCEHFCVNPDPGYSCECEGYRLAA 300
QY 318 DQRCBDDVDCILPSPCPQRCVNTQGFECCHCYPNYDLVDGECVBPVPCFRANCBYOC 377
DB 318 DQRCBDDVDCILPSPCPQRCVNTQGFECCHCYPNYDLVDGECVBPVPCFRANCBYOC 377
QY 301 DQRCBDDVDCILPSPCPQRCVNTQGFECCHCYPNYDLVDGECVBPVPCFRANCBYOC 360
DB 301 DQRCBDDVDCILPSPCPQRCVNTQGFECCHCYPNYDLVDGECVBPVPCFRANCBYOC 360
QY 378 QPLNQTSTYLCVCAEGFAPRPHBPHRCMPCNQTCAPADCBNTQASCECEGYILDDGFI 437
DB 378 QPLNQTSTYLCVCAEGFAPRPHBPHRCMPCNQTCAPADCBNTQASCECEGYILDDGFI 437
QY 361 QPLNQTSTYLCVCAEGFAPRPHBPHRCMPCNQTCAPADCBNTQASCECEGYILDDGFI 420
DB 361 QPLNQTSTYLCVCAEGFAPRPHBPHRCMPCNQTCAPADCBNTQASCECEGYILDDGFI 420
QY 438 CTDIDECENGFGSGVCHNLPGTFECICGPDALARIHIGTDCSGKVDGDSGSGEPPSP 497
DB 438 CTDIDECENGFGSGVCHNLPGTFECICGPDALARIHIGTDCSGKVDGDSGSGEPPSP 497
QY 421 CTDIDECENGFGSGVCHNLPGTFECICGPDALARIHIGTDCSGKVDGDSGSGEPPSP 480
DB 421 CTDIDECENGFGSGVCHNLPGTFECICGPDALARIHIGTDCSGKVDGDSGSGEPPSP 480
QY 498 PTPGSTLTPPAVGLVHSG 515
DB 498 PTPGSTLTPPAVGLVHSG 498

RESULT 13
US-08-312-870-3
Sequence 3, Application US/08312870
Patent No. 5639625
GENERAL INFORMATION:
APPLICANT: Carson, Craig W.
APPLICANT: Carson, Charles T.
TITLE OF INVENTION: Method for Detecting Antibodies to
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews

STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,870
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMRF B35150
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-312-870-3

Query Match 87.2%; Score 2793.5; DB 1; Length 497;
Best Local Similarity 99.4%; Pred. No. 1.6e-193;
Matches 494; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 19 AAPBPQSGSCVHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVISILLNGD 78
DB 1 AAPBPQSGSCVHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVISILLNGD 60
QY 79 GGVGRRLMIGLQLPFGCGDPKRLGRLGFWMTGDNNTSYSRRARLDLNGAPLCGPLCV 138
DB 61 GGVGRRLMIGLQLPFGCGDPKRLGRLGFWMTGDNNTSYSRRARLDLNGAPLCGPLCV 120
QY 139 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFHPATCRPLAVEPGAAAAVSIYGTPEFA 198
DB 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFHPATCRPLAVEPGAAAAVSIYGTPEFA 180
QY 199 ARGADFOALPVGSSAAVAFLGLQIMCTAPPGAVOGHMAREAPGAMDCSVENGGEHACNA 258
DB 181 ARGADFOALPVGSSAAVAFLGLQIMCTAPPGAVOGHMAREAPGAMDCSVENGGEHACNA 240
QY 259 IPGARPCCPAGALQADGRSCTAS-TOSCNLDCEHFCVNPDPDQGSYSCEMCEGYRLAA 317
DB 241 IPGARPCCPAGALQADGRSCTAS-TOSCNLDCEHFCVNPDPDQGSYSCEMCEGYRLAA 300
QY 318 DQHRCEVDVDCILBSPCPORCVNTQGGFEGCHCYPNYDLVDGECEVPEVDFRANCEYQC 377
DB 301 DQHRCEVDVDCILBSPCPORCVNTQGGFEGCHCYPNYDLVDGECEVPEVDFRANCEYQC 360
QY 378 QPLNQTSTLCVCAEGFAPRPHRRCQMFQNTACPADCDPNTQASCCEPGYIILDGFI 437
DB 361 QPLNQTSTLCVCAEGFAPRPHRRCQMFQNTACPADCDPNTQASCCEPGYIILDGFI 420
QY 438 CTDIDECENGFCSGVCHNLPGTFECICGPDALARHIGTDCDSKVDGSGSGSEPPPS 497
DB 421 CTDIDECENGFCSGVCHNLPGTFECICGPDALARHIGTDCDSKVDGSGSGSEPPPS 480
QY 498 PTPGSTLTTPPAVGLVHS 514
DB 481 PTPGSTLTTPPAVGLVHS 497

RESULT 14
US-09-331-793-4
Sequence 4, Application US/09331793

Patent No. 650646
GENERAL INFORMATION:
APPLICANT: KURIYAMA, Shinichi
APPLICANT: HASEGAWA, Takashi
TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
FILE REFERENCE: 1110-253P
CURRENT APPLICATION NUMBER: US/09/331,793
CURRENT FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patent version 3.0
SEQ ID NO 4
LENGTH: 497
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-331-793-4

Query Match 87.1%; Score 2789.5; DB 2; Length 497;
Best Local Similarity 99.2%; Pred. No. 3.1e-193; Indels 1; Gaps 1;
Matches 493; Conservative 0; Mismatches 3;

QY 19 AAPBPQSGSCVHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVISILLNGD 78
DB 1 AAPBPQSGSCVHDCFALYPGPATFLNASQICDGLRGLMTVRSSVAADVISILLNGD 60
QY 79 GGVGRRLMIGLQLPFGCGDPKRLGRLGFWMTGDNNTSYSRRARLDLNGAPLCGPLCV 138
DB 61 GGVGRRLMIGLQLPFGCGDPKRLGRLGFWMTGDNNTSYSRRARLDLNGAPLCGPLCV 120
QY 139 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFHPATCRPLAVEPGAAAAVSIYGTPEFA 198
DB 121 AVSAAEATVPSEPIWEEOQCEVKADGFLCEHFHPATCRPLAVEPGAAAAVSIYGTPEFA 180
QY 199 ARGADFOALPVGSSAAVAFLGLQIMCTAPPGAVOGHMAREAPGAMDCSVENGGEHACNA 258
DB 181 ARGADFOALPVGSSAAVAFLGLQIMCTAPPGAVOGHMAREAPGAMDCSVENGGEHACNA 240
QY 259 IPGARPCCPAGALQADGRSCTAS-TOSCNLDCEHFCVNPDPDQGSYSCEMCEGYRLAA 317
DB 241 IPGARPCCPAGALQADGRSCTAS-TOSCNLDCEHFCVNPDPDQGSYSCEMCEGYRLAA 300
QY 318 DQHRCEVDVDCILBSPCPORCVNTQGGFEGCHCYPNYDLVDGECEVPEVDFRANCEYQC 377
DB 301 DQHRCEVDVDCILBSPCPORCVNTQGGFEGCHCYPNYDLVDGECEVPEVDFRANCEYQC 360
QY 378 QPLNQTSTLCVCAEGFAPRPHRRCQMFQNTACPADCDPNTQASCCEPGYIILDGFI 437
DB 361 QPLNQTSTLCVCAEGFAPRPHRRCQMFQNTACPADCDPNTQASCCEPGYIILDGFI 420
QY 438 CTDIDECENGFCSGVCHNLPGTFECICGPDALARHIGTDCDSKVDGSGSGSEPPPS 497
DB 421 CTDIDECENGFCSGVCHNLPGTFECICGPDALARHIGTDCDSKVDGSGSGSEPPPS 480
QY 498 PTPGSTLTTPPAVGLVHS 514
DB 481 PTPGSTLTTPPAVGLVHS 497

RESULT 15
US-08-014-723-14
Sequence 14, Application US/08014723
Patent No. 5273962
GENERAL INFORMATION:
APPLICANT: Doi, Takeshi
APPLICANT: Iwasaki, Akio
APPLICANT: Saito, Yushi
APPLICANT: Kimura, Shigeru
APPLICANT: Onkuchi, Maeko
TITLE OF INVENTION: Thrombin-Binding Substance and Process
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C.

STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,723
FILING DATE: 19930208
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblion, No. 5273962man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-071-0 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEO ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-014-723-14

Query Match 85.4%; Score 2735.5; DB 1; Length 494;
Best Local Similarity 98.6%; Pred. No. 2.4e-189;
Matches 487; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY 1 MLGTVVIGALALAGGFAPAPAPPOGSGQCVHDCPALYPGPATFLNASQICDGLRGHLM 60
DB 1 MLGTVVIGALALAGGFAPAPAPPOGSGQCVHDCPALYPGPATFLNASQICDGLRGHLM 60
QY 61 TVRSSVADVISLILANGDGVGRRLMIQLQPPGCGDPKRLGPIRGFQWVTGDNNTSYS 120
DB 61 TVRSSVADVISLILANGDGVGRRLMIQLQPPGCGDPKRLGPIRGFQWVTGDNNTSYS 120
QY 121 RWARIDLNGAPLCGPLCAVAVSAEATVPSEPIWBEQCEVKADGFLCEFHFPATCRPLAV 180
DB 121 RWARIDLNGAPLCGPLCAVAVSAEATVPSEPIWBEQCEVKADGFLCEFHFPATCRPLAV 180
QY 181 EPGAAAALVSTYGTGPFARAGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHWRBAP 240
DB 181 EPGAAAALVSTYGTGPFARAGADFOALPVGSSAAVAPLGLQIMCTAPPGAVOGHWRBAP 240
QY 241 GAMDCSVENGCEHACNAIPGARPCQCPAGALQADGRSCTAS-TQSCNDLCEHFCVNP 299
DB 241 GAMDCSVENGCEHACNAIPGARPCQCPAGALQADGRSCTAS-TQSCNDLCEHFCVNP 299
QY 300 DQPGSYSCMCEGYRLADQHRCEVDVDCILPSPQRCVNTQGGFECHCYPNYDLVYG 359
DB 300 DQPGSYSCMCEGYRLADQHRCEVDVDCILPSPQRCVNTQGGFECHCYPNYDLVYG 359
QY 360 ECVREVDPCCFRANCYOCQPLNQTSYLCVCAEGFAPIPHEPRCOMFCNQTA CPADCDPN 419
DB 360 ECVREVDPCCFRANCYOCQPLNQTSYLCVCAEGFAPIPHEPRCOMFCNQTA CPADCDPN 419
QY 420 TQASCECEGYILDDGFICTDIDECENGAFCSGVCHNLPGTPECTCGPDSALVRHIGTDC 479
DB 420 TQASCECEGYILDDGFICTDIDECENGAFCSGVCHNLPGTPECTCGPDSALVRHIGTDC 479
QY 480 DSGKVDGDSGSGE 493
DB 480 DSGKVDGDSGSGE 493

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - protein search, using sw model

Run on: February 4, 2006, 04:24:42 ; Search time 246 Seconds

(without alignments)
1646.233 Million cell updates/sec

Title: US-10-725-013-2

Perfect score: 3203

Sequence: 1 MLGVLVIGALALAGLPPAP.....APSKKVLQHVTRTPTQRL 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3176.5	99.2	575	1 TRBM_HUMAN	P07204 homo sapien
2	3176.5	99.2	575	1 TRBM_SALIC	Q71U07 salmifl sci
3	3172.5	99.0	575	1 O81V29_HUMAN	O81V29 homo sapien
4	2317	72.3	578	1 TRBM_CANFA	O5W7P8 canis famli
5	2236	69.8	580	2 Q8H246_RABIT	Q8H246 oryctolagus
6	2113.5	66.0	577	1 TRBM_MOUSE	P15306 mus musculu
7	2113.5	66.0	577	1 O543W3_MOUSE	O543W3 mus musculu
8	2046.5	63.9	577	2 O8BJB5_MOUSE	O8BJB5 mus musculu
9	1799	56.2	491	2 O8BJB5_MOUSE	P97883 rattus norv
10	1600	50.0	461	2 TRBM_BOVIN	P06579 bos taurus
11	1314	41.0	356	1 TRBM_BOVIN	Q4SW52 tetradon n
12	651.5	20.3	496	2 Q4SW52_TESTING	Q4SW52 tetradon n
13	604.5	18.9	431	2 Q4SW52_TESTING	Q4SW52 tetradon n
14	597	18.6	671	2 O59EB6_HUMAN	O59EB6 homo sapien
15	590.5	18.4	652	1 C1QRI_HUMAN	O9NDY3 homo sapien
16	586.5	18.3	652	1 O81XK1_HUMAN	O81XK1 homo sapien
17	585	18.3	606	2 O5U4N0_XENLA	O5U4N0 xenopus lae
18	578	18.0	757	2 O9HCU0_HUMAN	O9HCU0 homo sapien
19	575	18.0	765	2 O91V98_MOUSE	O91V98 mus musculu
20	575	18.0	765	2 O91ZV1_MOUSE	O91ZV1 mus musculu
21	546	17.0	512	2 O4SW51_TESTING	O4SW51 tetradon n
22	545	17.0	644	1 C1QRI_MOUSE	O89103 mus musculu
23	531	16.6	643	1 C1QRI_RAT	O9E6E1 rattus norv
24	529.5	16.5	589	2 O4R1P1_TESTING	O4R1P1 tetradon n
25	481	15.0	136	2 O792T4_RAT	O792T4 rattus norv
26	426	13.3	1664	2 O9TVQ2_CABRL	O9TVQ2 caenorhabdi
27	414.5	12.9	1574	1 EGFL3_RAT	O88281 rattus norv
28	409.5	12.8	1277	2 O7RPG0_ANOGA	O7RPG0 anopheles g
29	398.5	12.4	1168	2 O6XCO_CABBR	O6XCO caenorhabdi
30	391	12.2	708	2 P87363_CHICK	P87363 gallus galli
31	386.5	12.1	1577	2 O9V589_DROME	O9V589 drosophila

32	384	12.0	2871	1 FBNI_BOVIN	P98133 bos taurus
33	384	12.0	2871	1 FBNI_HUMAN	P35555 homo sapien
34	384	12.0	2871	1 FBNI_PIG	O9CV36 sus scrofa
35	384	12.0	2871	2 O75N87_HUMAN	O75N87 homo sapien
36	384	12.0	3857	2 O88840_MOUSE	O88840 mus musculu
37	382	11.9	2871	1 FBNI_MOUSE	O61554 mus musculu
38	381.5	11.9	2225	2 O571J3_MOUSE	O571J3 mus musculu
39	378	11.8	1362	2 O559U0_DICDI	O559U0 dictyosteli
40	378	11.8	2884	2 O4SHN1_TESTING	O4SHN1 tetradon n
41	377.5	11.8	941	2 O54YP0_DICDI	O54YP0 dictyosteli
42	377	11.8	2872	2 O9WU8_RAT	O9WU8 rattus norv
43	376.5	11.8	2906	2 O9WU8_RAT	O9WU8 rattus norv
44	374.5	11.7	2907	1 FBNI_MOUSE	O61555 mus musculu
45	373.5	11.7	1976	2 O59ES6_HUMAN	O59ES6 homo sapien

ALIGNMENTS

RESULT 1

ID	TRBM_HUMAN	STANDARD	PRT	575 AA.
AC	P07204; Q9UC32;			
DT	01-APR-1988 (Rel. 07, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Thrombomodulin precursor (TM) (Fetomodulin) (CD141 antigen).			
GN	Name=THBD; Synonyms=THRM;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 19-43.			
RX	MEDLINE=8604395; PubMed=2820710;			
RA	Suzuki K., Kusumoto H., Deyashiki Y., Nishioaka J., Maruyama I.,			
RA	Zuehl M., Kawahara S., Honda G., Yamamoto S., Horiguchi S.;			
RT	"Structure and expression of human thrombomodulin, a thrombin receptor			
RT	on endothelium acting as a cofactor for protein C activation.";			
RL	EMBO J. 6:1891-1897(1987).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.			
RX	MEDLINE=86024950; PubMed=2822087;			
RA	Wen D., Dittman W.A., Ye R.D., Deaven L.L., Materus P.W., Sadler J.E.;			
RT	"Human thrombomodulin: complete cDNA sequence and chromosome			
RT	localization of the gene.";			
RL	Biochemistry 26:4350-4357(1987).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=87317665; PubMed=2819876;			
RA	Jackson R.W., Beeler D.L., Fritze L., Soff G., Rosenberg R.D.;			
RT	"Human thrombomodulin gene is intron depleted: nucleic acid sequences			
RT	of the cDNA and gene predict protein structure and suggest sites of			
RT	regulatory control.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:6425-6429(1987).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=88227901; PubMed=2836377;			
RA	Shirai T., Shiojiri S., Ito H., Yamamoto S., Kusumoto H.,			
RA	Deyashiki Y., Maruyama I., Suzuki K.;			
RT	"Gene structure of human thrombomodulin, a cofactor for thrombin-			
RT	catalyzed activation of protein C.";			
RL	J. Biochem. 103:281-285(1988).			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE (GENOMIC DNA), AND VARIANT VAL-473.			
RA	Rider M.J., Arnel T.Z., Carlington D.P., Chung M.-W., Lee K.L.,			
RA	Ozuna M., Poel C.L., Toch E.J., Yi O., Nickerson D.A.;			
RT	"Sequences, NHBI H16682 program for genomic applications, UM-			
RT	PHRCR, Seattle, WA (URL: http://pga.gs.washington.edu).";			
RL	Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.			
RN	[6]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			

RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/41865a;
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggaley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley C.P., Bird C.P., Blakey S.B., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Cooby N.R.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafton D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kap M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Kavanagh M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie I.J., McElay K., McMurtry A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showmken R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulterson J.B.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 [7]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marutina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Strepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uddin T.B., Toshyluki S., Carinini P., Prange C.,
 RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faley J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Bakerley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [8]
 RN CARBOHYDRATE-LINKAGE SITE SER-492, AND MUTAGENESIS.
 RP MEDLINE=94029900; PubMed=8216207;
 RX Gerlitz B., Hasegall T., Vlahos C.J., Parkinson J.F., Bang N.U.,
 RA Grinnell B.W.;
 RT "Identification of the predominant glycosaminoglycan-attachment site
 RT in soluble recombinant human thrombomodulin: potential regulation of
 RT functionality by glycosyltransferase competition for serine 474.";
 RL Biochem. J. 295:131-140(1993).
 [9]
 RN HYDROXYLATION OF ASN-342.
 RP MEDLINE=93293792; PubMed=8390446;
 RX Yamamoto S., Mizoguchi T., Tamaki T., Okuchi M., Kimura S., Aoki N.;
 RT "Urinary thrombomodulin, its isolation and characterization.";
 RL J. Biochem. 113:433-440(1993).
 [10]
 RN STRUCTURE BY NMR OF 389-407.
 RP MEDLINE=96007474; PubMed=7559494; DOI=10.1074/jbc.270.40.23366;
 RX Adler M., Seto W.H., Nitecki D.E., Lin J.H., Light D.R., Moser J.;
 RT "The structure of a 19-residue fragment from the C-loop of the fourth
 RT epidermal growth factor-like domain of thrombomodulin.";
 RL J. Biol. Chem. 270:23366-23372(1995).
 [11]
 RN STRUCTURE BY NMR OF 364-407.
 RP MEDLINE=96100636; PubMed=8528067;
 RX Meininger D.P., Hunter M.J., Komives E.A.;
 RT "Synthesis, activity, and preliminary structure of the fourth EGF-like
 RT domain of thrombomodulin.";
 RL Protein Sci. 4:1683-1695(1995).
 [12]
 RN STRUCTURE BY NMR OF 427-444.
 RP MEDLINE=95034791; PubMed=7947766;
 RX Srinivasan J., Hu S., Hrabal R., Zhu Y., Komives E.A., Ni F.;
 RT "Thrombin-bound structure of an EGF subdomain from human
 RT thrombomodulin determined by transferred nuclear Overhauser effects.";
 RL Biochemistry 33:13553-13560(1994).
 [13]
 RN STRUCTURE BY NMR OF 427-444.
 RP MEDLINE=96276211; PubMed=8745396;
 RX Hrabal R., Komives E.A., Ni F.;
 RT "Structural resiliency of an EGF-like subdomain bound to its target
 RT protein, thrombin.";
 RL Protein Sci. 5:195-203(1996).
 [14]
 RN STRUCTURE BY NMR OF 405-444.
 RP MEDLINE=98035729; PubMed=9367781; DOI=10.1006/jmbi.1997.1356;
 RX Sampoll Benitez B.A., Hunter M.J., Meininger D.P., Komives E.A.;
 RT "Structure of the fifth EGF-like domain of thrombomodulin: an EGF-like
 RT domain with a novel disulfide-bonding pattern.";
 RL J. Mol. Biol. 273:913-926(1997).
 [15]
 RN VARIANT TED TYR-486.
 RP MEDLINE=9511115; PubMed=7811989;
 RX Oehlin A.-K., Marlar R.A.;
 RT "The first mutation identified in the thrombomodulin gene in a 45-
 RT year-old man presenting with thromboembolic disease.";
 RL Blood 85:330-336(1995).
 [16]
 RN VARIANT TED TYR-486, AND VARIANTS THR-43, ALA-79, SER-495 AND LEU-501.
 RP MEDLINE=97341986; PubMed=9198186;
 RX Oehlin A.-K., Norlund L., Marlar R.A.;
 RT "Thrombomodulin gene variations and thromboembolic disease.";
 RL Thromb. Haemost. 78:396-400(1997).
 [17]
 RN VARIANT VAL-473.
 RP MEDLINE=97206518; PubMed=9157575;
 RX Norlund L., Holm J., Zoller B., Oehlin A.-K.;
 RT "A common thrombomodulin amino acid dimorphism is associated with
 RT myocardial infarction.";
 RL Thromb. Haemost. 77:248-251(1997).
 [18]
 RN VARIANT THR-43.
 RP MEDLINE=99057299; PubMed=9843165;
 RX Doggen C.J.M., Kunz G., Rosendaal F.R., Lane D.A., Vos H.L.,
 RA Stubbé P.J., Manger Cate V., Ireland H.;
 RT "A mutation in the thrombomodulin gene, 127G to A coding for Ala25thr,
 RT and the risk of myocardial infarction in men.";
 RL Thromb. Haemost. 80:743-748(1998).
 [19]
 RN VARIANT VAL-473.
 RP MEDLINE=21143723; PubMed=11245641;
 RX Wu K.K., Alekic N., Ann C., Boerwinkle E., Folsom A.R., Juneja H.;
 RT "Thrombomodulin Ala45Val polymorphism and risk of coronary heart
 RT disease.";
 RL Circulation 103:1386-1389(2001).
 [20]
 RN VARIANT TED TYR-486, AND VARIANT VAL-473.
 RP MEDLINE=22135346; PubMed=12137552;
 RX DOI=10.1046/j.1365-2141.2002.03644.x;
 RA Faloni E.M., Franchi F., Castaman G., Biguzzi E., Rodeghiero F.;
 RT "Mutations in the thrombomodulin gene are rare in patients with severe
 RT thrombophilia.";
 RL Br. J. Haematol. 118:595-599(2002).
 CC -!- FUNCTION: Thrombomodulin is a specific endothelial cell receptor

Query Match	99.2%	Score 3176.5	DB 1	Length 575
Best Local Similarity	99.5%	Pred. No. 7.2e-202		
Matches 572	Conservative 0	Mismatches 2	Indels 1	Gap 1
QY	1	MLGVLTGALALAGFPAPAPAPQDGSQCVEHDCFPALYPGATPLNLSQICDGLRHLM	60	
DB	1	MLGVLTGALALAGFPAPAPQDGSQCVEHDCFPALYPGATPLNLSQICDGLRHLM	60	
QY	61	TVRSVADVLSLLNGDGVGRRLMTGLQLPCCGPKLGLPLRGQWWTGDNNTSYS	120	
DB	61	TVRSVADVLSLLNGDGVGRRLMTGLQLPCCGPKLGLPLRGQWWTGDNNTSYS	120	
QY	121	RMARLDLNGAPLCCPLCAVNSAABATVSEBPTWESQCEVADGFLCEHPHATQPLAV	180	
DB	121	RMARLDLNGAPLCCPLCAVNSAABATVSEBPTWESQCEVADGFLCEHPHATQPLAV	180	
QY	181	EPGAAAAAVSTYGTFFPARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVGHAREAP	240	
DB	181	EPGAAAAAVSTYGTFFPARGADFOALPVGSSAAVAPLGLQMLCTAPPGAVGHAREAP	240	
QY	241	GAMDCSVENGCEHAQNAIPGARPCQCPAGALQADGSCITAS-TQSCNDLCEHFVCPNP	299	
DB	241	GAMDCSVENGCEHAQNAIPGARPCQCPAGALQADGSCITAS-TQSCNDLCEHFVCPNP	300	
QY	300	DQPSYSQMCCEGYRLADQRCHEVDCTLEPSPCPCPCVNTQGGFECHCVPNTDLDVG	359	
DB	301	DQPSYSQMCCEGYRLADQRCHEVDCTLEPSPCPCPCVNTQGGFECHCVPNTDLDVG	360	
QY	360	ECVEBPVDCFPANCFYOCQPLNQTSLCYCAEGFAPIPHEPHRCOMFCNQITACPADCPN	419	
DB	361	ECVEBPVDCFPANCFYOCQPLNQTSLCYCAEGFAPIPHEPHRCOMFCNQITACPADCPN	420	
QY	420	TQASCECEGYLLDDGFICTDIDECENGGFCGVCVCHNLPGTEPCTCGPDSALARIHGTDC	479	
DB	421	TQASCECEGYLLDDGFICTDIDECENGGFCGVCVCHNLPGTEPCTCGPDSALARIHGTDC	480	
QY	480	DSGVVDGSDSGSEPPSPPTGSLTTPPVGVLVHSGLLIGISIALCLVALLALLCHLR	539	
DB	481	DSGVVDGSDSGSEPPSPPTGSLTTPPVGVLVHSGLLIGISIALCLVALLALLCHLR	540	
QY	540	KKQGAARAKMEYKCAAPSEVVLQVTRTERPQRL	574	
DB	541	KKQGAARAKMEYKCAAPSEVVLQVTRTERPQRL	575	

RESULT 2

TRBM_SAISC

ID TRBM_SAISC STANDARD; PRT: 575 AA.

AC Q71U07;

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Thrombomodulin precursor (TM).

GN Name:THBD; Synonyms=TMSC;

OS Salimati scitureus (Common squirrel monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;

OC Cebinae; Salimati.

OX NCBI_TaxID=9521;

[1]

NP NUCLEOTIDE SEQUENCE.

RP Parzy D., Fuesel T., Torrentino M., Pouvelle B., Gysin J.,

RA "Salimati scitureus thrombomodulin gene."

RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.

CC -!- FUNCTION: Thrombomodulin is a specific endothelial cell receptor

CC that forms a 1:1 stoichiometric complex with thrombin. This

CC complex is responsible for the conversion of protein C to the

CC activated protein C (protein Ca). Once evolved, protein Ca

CC scissions the activated cofactors of the coagulation mechanism,

CC factor Va and factor VIIIa, and thereby reduces the amount of

CC	thrombin generated (By similarity).	
CC	-1- SUBCELLULAR LOCATION: Type 1 membrane protein (By similarity).	
CC	-1- PM: N-glycosylated (By similarity).	
CC	-1- SIMILARITY: Contains 1 C-type lectin domain.	
CC	-1- SIMILARITY: Contains 6 EGF-like domains.	
CC	-----	
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use as long as its content is in no way modified and this statement is not	
CC	removed.	
CC	-----	
CC	EMBL; AF169484; AAd49735.1; -; Genomic_DNA.	
DR	InterPro; IPR000152; Asx_hydroxy1_S.	
DR	InterPro; IPR000742; EGF_2.	
DR	InterPro; IPR001881; EGF_Ca bd.	
DR	InterPro; IPR006209; EGF-like.	
DR	InterPro; IPR006210; IEGF.	
DR	InterPro; IPR001304; Lectin_C.	
DR	InterPro; IPR001491; Thrombomodulin.	
DR	Pfam; PF00008; EGF; 2.	
DR	Pfam; PF00645; EGF_CA; 2.	
DR	Pfam; PF00059; Lectin_C; 1.	
DR	PRINTS; PR00907; THROMBOMODULN.	
DR	SMART; SM00034; CLECT; 1.	
DR	SMART; SM00181; EGF; 6.	
DR	SMART; SM00179; EGF_CA; 4.	
DR	PROSITE; PS00010; ASX_HYDROXYL; 2.	
DR	PROSITE; PS50041; C_TYPE_LECTIN_2; 1.	
DR	PROSITE; PS00022; EGF_1; FALSE_NEG.	
DR	PROSITE; PS01186; EGF_2; 2.	
DR	PROSITE; PS50026; EGF_3; 4.	
DR	PROSITE; PS01187; EGF_CA; 2.	
DR	Blood coagulation; EGF-like domain; Glycoprotein; Hydroxylation;	
KW	Receptor; Repeat; Signal; Transmembrane.	
FT	SIGNAL	1
FT	CHAIN	19
FT	TOPO_DOM	19
FT	TRANSMEM	516
FT	TOPO_DOM	540
FT	DOMAIN	31
FT	DOMAIN	241
FT	DOMAIN	284
FT	DOMAIN	325
FT	DOMAIN	365
FT	DOMAIN	404
FT	DOMAIN	441
FT	MOD_RS	342
FT	CARBOHYD	47
FT	CARBOHYD	115
FT	CARBOHYD	116
FT	CARBOHYD	382
FT	CARBOHYD	409
FT	CARBOHYD	490
FT	CARBOHYD	492
FT	DISULFID	245
FT	DISULFID	252
FT	DISULFID	267
FT	DISULFID	288
FT	DISULFID	292
FT	DISULFID	310
FT	DISULFID	329
FT	DISULFID	336
FT	DISULFID	351
FT	DISULFID	362
FT	DISULFID	378
FT	DISULFID	388
FT	DISULFID	390
FT	DISULFID	408
FT	DISULFID	417
FT	DISULFID	427
FT	DISULFID	445

FT DISUFID 451 464 By similarity.
 FT DISUFID 466 480 By similarity.
 SQ SEQUENCE 575 AA; 60329 MW; 9AF03CD151227D52 CRC64;
 Query Match 99.2%; Score 3176.5; DB 1; Length 575;
 Best Local Similarity 99.5%; Pred. No. 7.2e-202;
 Matches 571; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MLGVLVIGALALAGLPAPAPAPQPGSGQCYEHDCFLALPGPATFTLNASQICDGLRGLM 60
 DB 1 MLGVLVIGALALAGLPAPAPAPQPGSGQCYEHDCFLALPGPATFTLNASQICDGLRGLM 60
 QY 61 TVSSVADYVSLILNDGCGVGRRLWIGLQLPGCCDPKRLGRLRGFWTGNNTSYS 120
 DB 61 TVSSVADYVSLILNDGCGVGRRLWIGLQLPGCCDPKRLGRLRGFWTGNNTSYS 120
 QY 121 RMARLDINGAPLCPPLCVANSAATVPSEPIWEEOCEVADDFLCFHFPPATCRPLAV 180
 DB 121 RMARLDINGAPLCPPLCVANSAATVPSEPIWEEOCEVADDFLCFHFPPATCRPLAV 180
 QY 181 EPGAAAASVITTYGTPFAARGADPQALPVGSSAAVAPLGLQLMCTAPPGAVQGHMAREAP 240
 DB 181 EPGAAAASVITTYGTPFAARGADPQALPVGSSAAVAPLGLQLMCTAPPGAVQGHMAREAP 240
 QY 241 GAMDSCYENGCCEHACNAIPGAPPCQCPAGALQADRSCTAS-TQSCNDLCFHFVCPNP 299
 DB 241 GAMDSCYENGCCEHACNAIPGAPPCQCPAGALQADRSCTAS-TQSCNDLCFHFVCPNP 299
 QY 300 DQPSYSCKETGYRLAADHRCEDVDCCIIEPSPCPCRCVNTQGGFCHCYPNYDLVDG 359
 DB 301 DQPSYSCKETGYRLAADHRCEDVDCCIIEPSPCPCRCVNTQGGFCHCYPNYDLVDG 360
 QY 360 ECVBPVPCFRANCEYOCQPLNQTSTYLCVCAEGFAP1PHEBHCQMFNCQACPADCPN 419
 DB 361 ECVBPVPCFRANCEYOCQPLNQTSTYLCVCAEGFAP1PHEBHCQMFNCQACPADCPN 420
 QY 420 TQASCECEGTYLDDGFTCTDIDECENGFCSCVCANLPGTFECICGPDALAHIGTDC 479
 DB 421 TQASCECEGTYLDDGFTCTDIDECENGFCSCVCANLPGTFECICGPDALAHIGTDC 480
 QY 480 DSGVVDGDSGSGSPSPGSLTPPAVGLVHSGILIGISIASLCLVALLALCLHLR 539
 DB 481 DSGVVDGDSGSGSPSPGSLTPPAVGLVHSGILIGISIASLCLVALLALCLHLR 540
 QY 540 KKGGAARAKMEYKCAAPSKEVVLQHVTERTPORL 574
 DB 541 KKGGAARAKMEYKCAAPSKEVVLQHVTERTPORL 575

RESULT 3
 Q8IV29 HUMAN PRELIMINARY; PRT; 575 AA.
 ID Q8IV29
 AC Q8IV29
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Thrombomodulin.
 GN Name:THBD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Scheffen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datschenko L., Marutina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaant T.T., Scheetz T.E.,

RA Brownstein M.J., Uedin T.B., Toohyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loguolino N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boek S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Moxley K.C., Hale S., Garcia A.M., Gay L.D., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalek U., Smalhus D.E.,
 RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RG NIH MGC Project;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC035602; AAH35602.2; -; mRNA.
 DR HSSP; P07204; 12AQ.
 DR Ensembl; ENSG00000178726; Homo sapiens.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0007596; P:blood coagulation; IEA.
 DR InterPro; IPR001521; Aex_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca_bd.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR001491; Thrombomodulin.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF07645; EGF CA; 2.
 DR Pfam; PF00059; Lectin C; 1.
 DR PRINTS; PR00307; THROMBOMODULN.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00181; EGF; 6.
 DR SMART; SM00179; EGF CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 2.
 DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS50026; EGF_3; 4.
 DR PROSITE; PS01187; EGF CA; 2.
 SQ SEQUENCE 575 AA; 60357 MW; 9252B6F9E01963AC CRC64;
 Query Match 99.0%; Score 3172.5; DB 2; Length 575;
 Best Local Similarity 99.3%; Pred. No. 1.3e-201;
 Matches 571; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MLGVLVIGALALAGLPAPAPAPQPGSGQCYEHDCFLALPGPATFTLNASQICDGLRGLM 60
 DB 1 MLGVLVIGALALAGLPAPAPAPQPGSGQCYEHDCFLALPGPATFTLNASQICDGLRGLM 60
 QY 61 TVSSVADYVSLILNDGCGVGRRLWIGLQLPGCCDPKRLGRLRGFWTGNNTSYS 120
 DB 61 TVSSVADYVSLILNDGCGVGRRLWIGLQLPGCCDPKRLGRLRGFWTGNNTSYS 120
 QY 121 RMARLDINGAPLCPPLCVANSAATVPSEPIWEEOCEVADDFLCFHFPPATCRPLAV 180
 DB 121 RMARLDINGAPLCPPLCVANSAATVPSEPIWEEOCEVADDFLCFHFPPATCRPLAV 180
 QY 181 EPGAAAASVITTYGTPFAARGADPQALPVGSSAAVAPLGLQLMCTAPPGAVQGHMAREAP 240
 DB 181 EPGAAAASVITTYGTPFAARGADPQALPVGSSAAVAPLGLQLMCTAPPGAVQGHMAREAP 240
 QY 241 GAMDSCYENGCCEHACNAIPGAPPCQCPAGALQADRSCTAS-TQSCNDLCFHFVCPNP 299
 DB 241 GAMDSCYENGCCEHACNAIPGAPPCQCPAGALQADRSCTAS-TQSCNDLCFHFVCPNP 300
 QY 300 DQPSYSCKETGYRLAADHRCEDVDCCIIEPSPCPCRCVNTQGGFCHCYPNYDLVDG 359

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Db 301 DQPSGSCMCEGTYLAADQHRCEVDVDCILPSPSCPCRCVNTQGGFECHCYPNTDLYDGG 360
Oy 360 ECVEVDPCFRANCEGOCOPLNQSYLVCYCAEGFAPIPHEPRRCMPFCNQTCAPADCPDN 419
Db 361 ECVEVDPCFRANCEGOCOPLNQSYLVCYCAEGFAPIPHEPRRCMPFCNQTCAPADCPDN 420
Oy 420 TQASCECEGYILDDGFICTDIDECENGFCGVCCHNLPGTEPCI CGPDSALARHIGTDC 479
Db 421 TQASCECEGYILDDGFICTDIDECENGFCGVCCHNLPGTEPCI CGPDSALVRHIGTDC 480
Oy 480 DSGKVDGSDSGSGEPSPSTPTLTPPAVGVHSGLLIGISLCLVALLALCHLR 539
Db 481 DSGKVDGSDSGSGEPSPSTPTLTPPAVGVHSGLLIGISLCLVALLALCHLR 540
Oy 540 KKGARARAMEYKCAAPSKEVVLQHVTRTERPQRL 574
Db 541 KKGARARAMEYKCAAPSKEVVLQHVTRTERPQRL 575

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RESULT 4

```

TRBM_CANPA
ID TRBM_CANPA STANDARD; PRT; 578 AA.
AC QSW7B8;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Thrombomodulin precursor (TM).
GN Name=THBD;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OC NCBI_TaxID=9615;
OX [1]
RN NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
RX PubMed:15585960;
RA Maruyama H., Ogura K., Maeda S., Kano R., Tsujimoto H., Watari T.,
RA Tokuriki M., Hasegawa A.;
RT "Molecular cloning of canine thrombomodulin cDNA and expression in
RT normal tissues."
RT J. Vet. Med. Sci. 66:1423-1427(2004).
CC -1- FUNCTION: Thrombomodulin is a specific endothelial cell receptor
CC that forms a 1:1 stoichiometric complex with thrombin. This
CC complex is responsible for the conversion of protein C to the
CC activated protein C (protein Ca). Once evolved, protein Ca
CC activates the activated cofactors of the coagulation mechanism,
CC factor Va and factor VIIIa, and thereby reduces the amount of
CC thrombin generated (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- TISSUE SPECIFICITY: Expressed in lung, liver, spleen, kidney,
CC pancreas and lymph node. Low expression in heart, cerebrum,
CC urinary bladder and uterus.
CC -1- PTM: N-glycosylated (By similarity).
CC -1- SIMILARITY: Contains 1 C-type lectin domain.
CC -1- SIMILARITY: Contains 6 EGF-like domains.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AB193481; BAD6823.1; -; mRNA.
DR InterPro; IPR000152; Asx_Hydroxy1_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR001491; TmrbModuLn.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF07645; EGF_CA; 1.

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DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00907; THRMOMODULN.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 6.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS50026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 2.
DR Blood coagulation; EGF-like domain; Glycoprotein; Hydroxylation;
KW Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 16
FT CHAIN 17 578
FT TOPO_DOM 17 518
FT TRANSMEM 519 539
FT TOPO_DOM 540 578
FT DOMAIN 31 167
FT DOMAIN 242 282
FT DOMAIN 285 325
FT DOMAIN 326 364
FT DOMAIN 366 406
FT DOMAIN 405 441
FT DOMAIN 442 481
FT MOD_RES 343 343
FT CARBOHYD 114 114
FT CARBOHYD 300 300
FT CARBOHYD 410 410
FT CARBOHYD 493 493
FT CARBOHYD 495 495
FT DISULFID 246 257
FT DISULFID 253 266
FT DISULFID 268 281
FT DISULFID 289 297
FT DISULFID 293 309
FT DISULFID 311 324
FT DISULFID 330 341
FT DISULFID 337 350
FT DISULFID 352 363
FT DISULFID 370 379
FT DISULFID 375 389
FT DISULFID 391 405
FT DISULFID 409 414
FT DISULFID 418 426
FT DISULFID 428 440
FT DISULFID 446 455
FT DISULFID 451 464
FT DISULFID 466 480
SQ SEQUENCE 578 AA; 60745 MW; 06D255C9B8FC0883 CRC64;

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Query Match 72.3%; Score 2317; DB 1; Length 578;
 Best Local Similarity 73.2%; Pred. No. 4,9e-145;
 Matches 426; Conservative 44; Mismatches 100; Indels 12; Gaps 8;

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Oy 1 MGVLVVIGALALAGLGPAPAPPEPQSGSCYEHDCFPALYPGPATFLNASQICDGLRGLM 60
Db 1 MLRVTLGLVLAIPAGIGLPTPAQPPRSQCEHDCFOLEFRGPATFLAASQCCEGIGHLM 60
Oy 61 TVRSSVADVTSILNDGCVGRRLWTGLQTPPGCCDPRKLGFLRGQVWTGNNNTSYS 120
Db 61 TVRSSVADVTSILNDGCVGRRLWTGLQTPPGCCDPRKLGFLRGQVWTGNNNTSYS 119
Oy 121 RWARLDLNGA-PLCGPLCVAAVAEAATVSEPIWEBOCEVKAADGFLCEFFHPATCRPIA 179
Db 120 RWARPHVGPAAPPCAPLCVANSDDAAAPAPGEPMAEBGRCAEAADGFLCEFFHPASCRPL 179
Oy 180 VEPGAAAA-VSTYGGPPPAARGADFOALPYGSSAAVAAPLGLQLMCTAPGCAVGGHARE 238
Db 180 VDAARAAAAAGVSTYTPFGARGADFOALPYGSSAAVAAPFGVQLACAPRGEAEARWGRE 239

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QY 239 APGAMDCSVENGGCEHACNAIPGARPCCCPAGAAIQAADGRSC-TASTOSCNLDCEHFCVP 297
DB 240 APGAMDCSVENGGCGORACSAGAPRLCLCPADYIQAADGRSCATFAHSCCHKCEHFCIP 299
QY 298 NPDDPGSYSCMCEGYRLAAOHCEBDVDDCILBSPRCQVNTQGGFEGHCYPNYDLV 357
DB 300 NASVGSYLCCEGYRLAQAHRCEBDVDDCIQVPSLCPQLCVNTRGAFEGHCYGYELV 359
QY 358 DGECEVPDPCFRANCEYQCCPLNQTSTYLCVCAEGFAPRIPHEPHRCQMFNCQTACPADCD 417
DB 360 DNECEVPDPCFGSKCEYQCCPVSGTQRCICAGSFAPVPHDPHRCQMFNCQTACPADCD 419
QY 418 PNTQASCCEPBGYIILDDGFICTDIDECENGGFCSCVCHNLPGTPECTCGPDSALARIHGT 477
DB 420 PNSTPSCQCPBGYIILDDGFICTDIDECENGE-CEPACNLTPEGYECTCGPDSPLAGQVAT 478
QY 478 DCDGSKV---DG-DGSGSGPPSPPTPGSTLTTPAVGLVHSGILIGISIASLCLVVAL 532
DB 479 DC--GRITSDPDGSDSGSEPPVTPPTGVTSPSPVPVSHGVILIGISIASLCLVVAL 536
QY 533 ALLCHLRKKGGAARAKMEYKCAAPSKKEVVLQHVRTERTPORTL 574
DB 537 ALLCHLRKKGGAARAKMEYKCAAPSKKEVVLQHVRTERTPORTL 578

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RESULT 5
Q8H248 RABIT PRELIMINARY; PRT; 580 AA.
AC Q8H248
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Thrombomodulin precursor.
GN Name=Thbd;
OS Oryctolagus cuniculus (Rabbit).
OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelaeostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:15018348; DOI=10.1080/10425170310001608416;
RA Deng J.B., Kim A.Y., Bian C.E., Regard J.B., Rade J.J.;
RT "CDNA cloning of rabbit thrombomodulin and characterization of gene
RT expression in cardiovascular tissue.";
RL DNA Seq. 14:399-405(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Deng J.B., Kim A.Y., Rade J.J.;
RT "Cloning of rabbit thrombomodulin cDNA sequence.";
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PROTEIN SEQUENCE.
RX PubMed:2536746;
RA Stearns D.J., Kurosawa S., Esmen C.T.;
RT "Microthrombomodulin. Residues 310-486 from the epidermal growth
RT factor precursor homolog domain of thrombomodulin will accelerate
RT protein C activation.";
RL J. Biol. Chem. 264:3352-3356(1989).
DR EMBL; AY138902; AAN15931.2; -, mRNA.
DR PIR; A33308; A33308.
DR HSSP; P07204; 1TKR.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005528; F:sugar binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR001304; Lectin_C.

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DR InterPro; IPR002919; Prot. Inh. CR_TIL.
DR InterPro; IPR001491; Thrombomodulin.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF07645; EGF_CA_1.
DR Pfam; PF00059; Lectin_C_1.
DR PRINTS; PR00907; THROMBOMODULN.
DR SMART; SM00034; CLECT_1.
DR SMART; SM00179; EGF_CA_1.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS50026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA_2.
KW Signal.
FT SIGNAL
SQ SEQUENCE 580 AA; 60116 MW; ABA328FD2E11FA2 CRC64;

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Query Match 69.8%; Score 2236; DB 2; Length 580;
Best local similarity 72.0%; Pred. No. 1,1e-139;
Matches 417; Conservative 35; Mismatches 107; Indels 20; Gaps 9;

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QY 4 VLVIQALALAGIAPAPAPAPAPQPGSQCVYHDCFALYPPATFELNASQICDGLRGLMTVR 63
DB 6 LLLIGALAPAGIGLPTNAEPQDGSQCVYHDCFALYPPATFELNASQICDGLRGLMTVR 65
QY 64 SSVADVYSLINDGCVGRRLWITGLQPPGCCDPRKLGPRGFWYTGNNTSYSRWA 123
DB 66 SSVADVYSLINDGCVGRRLWITGLQPPGCCDPRKLGPRGFWYTGNNTSYSRWA 121
QY 124 RLDINGAPVLCPLCYAASAEATVSEPIWEQCEVADSFLEFHEPATCRPLAVBP 183
DB 122 RODGGAPVYCPVYSAASAAAPGEPAMELTCGRVDFLEFHEPATCRPLAVBP 181
QY 184 AAAAA--VSITYGTPAARGADFOALPVSSAAVAPLGLQMTAPPGAVQGHKARAP 240
DB 182 AAPATAPVSVSTYSTPFGARADFOALPVSSAAVAPLGLQMTAPPGAVQGHKARAP 241
QY 241 GAMDCSVNCGCEHACNAIPGARPCQCPAGAAIQAADGSC-TASTOSCNLDCEHFCVNP 299
DB 242 GAMDCSVNCGCEHACNAIPGARPCQCPAGAAIQAADGSC-TASTOSCNLDCEHFCVNP 301
QY 300 DPGSYSCMCEGYRLAQAHRCEBDVDDCILBSPRCQVNTQGGFEGHCYPNYDLV 359
DB 302 DASGYSCMCEGYRLAQAHRCEBDVDDCILBSPRCQVNTQGGFEGHCYPNYDLV 361
QY 360 ECVPEVDPCEFRANCEYQCCPLNQTSTYLCVCAEGFAPRIPHEPHRCQMFNCQTACPADCPN 419
DB 362 ECVPEVDPCEFRANCEYQCCPLNQTSTYLCVCAEGFAPRIPHEPHRCQMFNCQTACPADCPN 420
QY 420 TQASCCEPBGYIILDDGFICTDIDECENGGFCSCVCHNLPGTPECTCGPDSALARIHGT 479
DB 421 YPSTLCPEBGYIILDDGFICTDIDECENGGFCSCVCHNLPGTPECTCGPDSALARIHGT 479
QY 480 -----DSGKVDG--DSGSGSPSPPTPGST-LTPPAVGLVHSGILIGISIASLCLVVAL 531
DB 480 YPTQVSDG--DGGDGGSGSPSPPTPGST-LTPPAVGLVHSGILIGISIASLCLVVAL 537
QY 532 LALLCHLRKKGGAARAKMEYKCAAPSKKEVVLQHVRTERT 570
DB 538 LALLCHLRKKGGAARAKMEYKCAAPSKKEVVLQHVRTERT 576

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RESULT 6
ID TRBM_MOUSE STANDARD; PRT; 577 AA.
AC P15306;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thrombomodulin precursor (TM) (Fetomodulin).
GN Name=Thbd;
OS Mus musculus (Mouse).
OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelaeostomi;

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OC Mammalia; Euteria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OX Muroidea; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=89128454; PubMed=2536925;
RA Dittman W.A., Majerus P.W.;
RT "Sequence of a cDNA for mouse thrombomodulin and comparison of the
RT predicted mouse and human amino acid sequences.";
RL Nucleic Acids Res. 17:802-802(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=8908498; PubMed=2844823;
RA Dittman W.A., Kumada T., Sadler J.E., Majerus P.W.;
RT "The structure and function of mouse thrombomodulin. Phorbol myristate
RT acetate stimulates degradation and synthesis of thrombomodulin without
RT affecting mRNA levels in hemangioma cells.";
RL J. Biol. Chem. 263:15815-15822(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX STRAIN=Czech II; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tshibkyti S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Riksteley K.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Thrombomodulin is a specific endothelial cell receptor
CC that forms a 1:1 stoichiometric complex with thrombin. This
CC complex is responsible for the conversion of protein C to the
CC activated protein C (protein Ca). Once evolved, protein Ca
CC activates the activated cofactors of the coagulation mechanism,
CC factor Va and factor VIII, and thereby reduces the amount of
CC thrombin generated.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Endothelial cells are unique in synthesizing
CC thrombomodulin (By similarity).
CC -1- SIMILARITY: Contains 1 C-type lectin domain.
CC -1- SIMILARITY: Contains 6 EGF-like domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X14432; CA432597.1; -; mRNA.
DR EMBL; BC019154; AAH19154.1; -; mRNA.
DR PIR; S08488; A60501.
DR HSP; P07204; 1SGT.
DR MG; MG198736; Thbd.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0007596; P:blood coagulation; TAS.
DR GO; GO:0009790; P:embryonic development; IMP.
DR GO; GO:0050819; P:negative regulation of coagulation; TAS.
DR GO; GO:0007565; P:pregnancy; IMP.

DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR001491; Thrombomodulin.
DR Pfam; PF00008; EGF 1.
DR Pfam; PF07645; EGF_Ca 1.
DR Pfam; PF00059; Lectin C 1.
DR PRINTS; PR00907; THROMBOMODULIN.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_Ca 1.
DR PROSITE; PS00010; ASX_HYDROXYL 2.
DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
DR PROSITE; PS00022; EGF 1; FALSE_NEG.
DR PROSITE; PS01186; EGF 2; 3.
DR PROSITE; PS00026; EGF 3; 3.
DR PROSITE; PS01187; EGF_Ca 2.
KW Blood coagulation; EGF-like domain; Glycoprotein; Receptor; Repeat;
KW Signal; Transmembrane.
FT SIGNAL 1 16
FT CHAIN 1 577
FT TOPO_DOM 17 517
FT TRANSMEM 518 541
FT TOPO_DOM 542 577
FT DOMAIN 31 167
FT DOMAIN 240 280
FT DOMAIN 283 323
FT DOMAIN 324 362
FT DOMAIN 364 404
FT DOMAIN 403 439
FT DOMAIN 440 480
FT CARBOHYD 113 113
FT CARBOHYD 243 243
FT CARBOHYD 256 256
FT CARBOHYD 408 408
FT CARBOHYD 494 494
FT DISULFID 244 255
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FT DISULFID 266 279
FT DISULFID 287 295
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FT DISULFID 389 403
FT DISULFID 407 416
FT DISULFID 412 424
FT DISULFID 426 438
FT DISULFID 444 454
FT DISULFID 449 463
FT DISULFID 465 479
FT SEQUENCE 577 AA; 6186 MW; B20E50B0E745014 CRC64;
Query Match 66.0%; Score 2113.5; DB 1; Length 577;
Best Local Similarity 67.0%; Pred. No. 1.4e-131;
Matches 388; Conservative 53; Mismatches 129; Indels 9; Gaps 5;
OY 1 MLGLVILGALALAGFPAPAPRPGSGQCYEHHCPLXPRAPFVNASQICDGLRGILM 60
DB 1 MLGLFPGVLPALVGLSALAKLQPTGSCQYEHHCPLFGQPAFLDASQCRLOGHLM 60
OY 61 TVRSSVADYVILSLINDG-GVGRRLWTIGLPLPGCGDPRGLPLRGFQWVTDNNTSY 119
DB 61 TVRSSVADYVILSLSSNDLGP---WIGLQLPGQCDPRVHLGPLGFGWVTDNNTSY 117
OY 120 SRWRLDLNAPLGLCPICVAASAATVPSPPIWEBOQCEVKADGFLCEHFPATCPPLA 179
DB 118 SRWARPNDQFAPLCPGLCVTVSTATEAAPGPAPWEKRCETETGFLCEFYFTASCRPLT 177

QY 180 VEP-GAAAAVSTYGTFFARAGADFQALPVGSSAAVAPLQIMCTAPGAVOGHWARE 238
 DB 178 VNRDPERAAHISSTYNTPFVGSADPQLPVGSSAAVAPLQELVCRAPPTSGHWAME 237
 QY 239 APGAMDCSVENGCEHACNAIPGARPCCCPAGALQADGSCYAS-TGSCNDLCEHFVCP 297
 DB 238 ATGAMNCSVENGCCEYLGNRSTNEPRCLCPRDMQLQADGRSCAPVWVQSCNELCEHFVCS 297
 QY 298 NPDPGSGSCMCEGYRLAADOHCEBDVDCILBSPCPCRCVMTQGFCEHCYPNVLY 357
 DB 298 NAEVPGSISCMCEGYRLAADOHCEBDVDCILBSPCPCRCVMTQGFCEHCYPNVLY 357
 QY 358 DGECEVPCFRANACEYQCCPLNQTSTYLCVCAEGFAP1PHEPRCQMFNCQTAACPADCD 417
 DB 358 DGECEVPCFRANACEYQCCPLNQTSTYLCVCAEGFAP1PHEPRCQMFNCQTAACPADCD 417
 QY 418 PNTQASCCEPGYILDDGFTCTDIDECENGGFCGVCNLTETPCTCTGPPSALAHGT 477
 DB 418 PNTQASCCEPGYILDDGFTCTDIDECENGGFCGVCNLTETPCTCTGPPSALAHGT 477
 QY 478 DCDGSGV---DGGDSGSGEPPTPGSTLTPPAVGLVHSGLLGISIASICLVVALLAL 534
 DB 478 DCDGSGV---DGGDSGSGEPPTPGSTLTPPAVGLVHSGLLGISIASICLVVALLAL 534
 QY 535 LCHLRKQGAARAKMEYKCAAPSKVVLQHVARTERTPOR 573
 DB 535 LCHLRKQGAARAKMEYKCAAPSKVVLQHVARTERTPOR 573
 QY 573 LCHLRKQGAARAKMEYKCAAPSKVVLQHVARTERTPOR 573
 DB 573 LCHLRKQGAARAKMEYKCAAPSKVVLQHVARTERTPOR 573
 RESULT 7
 ID 0543W3_MOUSE PRELIMINARY; PRT; 577 AA.
 AC 0543W3_MOUSE PRELIMINARY; PRT; 577 AA.
 DT 13-SEP-2005 (TRENBLrel. 31, Created)
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
 DE 9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched
 DE library, clone:B130014A08 product:THROMBOMODULIN (PETOMODULIN) (TM),
 DE full insert sequence (Thbd protein).
 GN Name=Thbd;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=21085660; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Kanai A., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glass C., King B., Kochi H.,
 RA Kuehl P., Lewis S., Matsumoto Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Steubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baladrelli R., Bash G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guerninich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Notone F., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,

RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kanaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=22354683; PubMed=12468851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,
 RA Nikaido I., Oseko N., Saito R., Suzuki H., Yamana K., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schenbach C., Gojobori T.,
 RA Baladrelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanaji A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad T., Brusio V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Glass C., Godzik A., Gough J.,
 RA Grimmond S., Guerninich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kanaji H., Kawaasa Y., Kodzierski R.M., King B.L.,
 RA Kanaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Marchionni L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Petter G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.V., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Savelin A., Schneider C., Sempole C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Walstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszew-Boris A., Yanagisawa M., Yang L., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Maki K., Kawai K., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama N., Nishine T., Harada A.,
 RA Yamamoto S., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wachihi K.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multiplexed sequencing."
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Koda M., Koya S.,
 RA Kurihara C., Matsumoto T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RA Ebert L., Muenstermann E., Schatten R., Henze S., Bohn E.,
 RA Mollenhauer J., Wiemann S., Schick M., Korn B.,
 RT "Cloning of mouse full open reading frames in Gateway(R) system entry
 vector (pDONR201)."
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK044928; BAC32146.1; -; mRNA.
 DR EMBL; CT010375; CAJ18582.1; -; mRNA.
 DR MGI; MGI:98735; Thbd.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0005866; C:plasma membrane; TAS.
 DR GO; GO:0007596; P:blood coagulation; TAS.
 DR GO; GO:0009790; P:embryonic development; IMP.
 DR GO; GO:0050819; P:negative regulation of coagulation; TAS.
 DR GO; GO:0007565; P:pregnancy; IMP.
 DR InterPro; IPR000152; Asx_hydroxyl_5.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca_bd.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR001491; Thrombomodulin.
 DR Pfam; PF00008; EGF_1.
 DR Pfam; PF07645; EGF_CA_1.
 DR Pfam; PF00059; Lectin_C_1.
 DR PRINTS; PR00907; THROMBOMODULIN.
 DR SMART; SM00034; CLECT_1.
 DR SMART; SM00181; EGF_6.
 DR SMART; SM00179; EGF_CA_4.
 DR PROSITE; PS00010; ASX_HYDROXYL_2.
 DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS50026; EGF_3; 3.
 DR PROSITE; PS01187; EGF_CA_2.
 DR PROSITE; PS01187; EGF_CA_2.
 SQ SEQUENCE 577 AA; 61868 MW; B20E50B0FE745014 CRC64;
 Query Match 66.0%; Score 2113.5; DB 2; Length 577;
 Best Local Similarity 67.0%; Pred. No. 1.4e-131;
 Matches 388; Conservative 53; Mismatches 129; Indels 9; Gaps 5;
 QY 1 MLGVLTALATAGLPAPAPAPGSGSQVCEHDFALPYGPATLNASQICDGRGILM 60
 DB 1 MLGIFGLVLAAPASIGLALATLQPTGSCVHEGCFALFGGATLIDASQACORLQGHLM 60
 QY 61 TVRSSVAADVLSLLINGDG-GVGRRLWIGLQLPQCCGDPKLGFLRGFQWVTGDNNTSY 119
 DB 61 TVRSSVAADVLSLLINGDG-GVGRRLWIGLQLPQCCGDPKLGFLRGFQWVTGDNNTSY 117
 QY 120 SRMARLDNGAPLCPGLCVAVSAARATVPSEPIWEEQCEVADGFLCEHFPATCRPLA 179
 DB 118 SRMARPNQOTAPLCPGLCVATVSTATEAAPGEPAMWKEKCEETQGLCEHFPATCRPLT 177
 QY 180 VEP-GAAAAVSYITGTFFPAARAGADFOALPVGSSAAVPLIGLQIACTAPGAVQGMAR 238
 DB 178 VNTADPEAAHISSTNTPTFGVSGADFOALPVGSSAAVPLIGLQIACTAPGAVQGMAR 237
 QY 239 AFGAWDCSVENGCGCHACNAIPGARPCQCPAGALQADGRSCTAS-TOSCNDCHEFCVP 297
 DB 238 ATGAWNCSEVNGGCEYLGNRSITNEPRCLCPRMMDLQADGRSARAVVGSCHNLCHEFCVS 297
 QY 298 NPDPGASISCMCEITGYRLAADHREEDVDDCTLESPQRCQVNTQGGRECHCYNYDLY 357
 DB 298 NAEVGSYSYCMCEITGYRLAADHREEDVDDCKQGNPCPOLCVNTKGGRECHCYNYDLY 357
 QY 358 DGECEVAPDPCFRANCEYQCCPLNQTYSYLCVCAEGFAPLPIPHRCONFCNQTACPAD 417
 DB 358 DGECEVAPDPCFRANCEYQCCPLNQTYSYLCVCAEGFAPLPIPHRCONFCNQTACPAD 417
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DB 418 PNTQASCECPREGYILDGFTCTDIDECENGFCGVCVCHNLPTGPECICGPDALARIHGT 477
 QY 478 DCDGSKV---DCGDSGSGGPPSPPTPGSTLTPAVGLVSGLLIGISLALCVVALLAL 534
 DB 478 DCDPFPVEDTTEEGSGSGPPSPPTPGSTLTPAVGLVSGLLIGISLALCVVALLAL 537
 QY 535 LCHLRKKGGAARAKMEYKCAAPSKEVVLQHVTEPTPQR 573
 DB 538 LCHLRKKGGAARAKMEYKCAAPSKEVVLQHVTEPTPQR 576
 RESULT 8
 O35370_RAT PRELIMINARY; PRT; 577 AA.
 AC O35370;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 10-MAY-2005 (TREMblrel. 30, Last annotation update)
 DB Thrombomodulin.
 GN Name=Thbd;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 ON NCBI_Taxid=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Lung;
 RX MEDLINE=99246062; PubMed=10231031;
 RA Wang J., Yao A., Wang J.Y., Sung C.C., Fink L.M., Hardin J.W.,
 RA Hauer-Jensen M.;
 RT "cdna cloning and sequencing, gene expression, and immunolocalization
 of thrombomodulin in the Sprague-Dawley rat.";
 RL DNA Res. 6:57-62(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Martulina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrini P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Keltman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska J., Smalios D.E.,
 RA Scherch A., Schein J.R., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RA Straube R.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF022743; AAB80760.1; -; mRNA.
 DR EMBL; BC070903; AAB70903.1; -; mRNA.
 DR HSSP; P07204; 1FGD.
 DR Ensembl; ENSRNOG0000004687; Rattus norvegicus.
 DR RGD; 621299; Thbd.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.


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RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Koyama M., Koyama S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Niishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saeki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RA Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK089479; BAC40898.1; -; mRNA.
DR HSSP; P07204; 1FGD.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR00152; Asx hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR001491; Thrombomodulin.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF07645; EGF_Ca; 1.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00907; THROMBOMODULIN.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_Ca; 1.
DR PROSITE; PS00010; ASX_HYDROXYL_2.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS50026; EGF_3; 3.
DR PROSITE; PS01187; EGF_Ca; 2.
DR NON TER 491
SQ SEQUENCE 491 AA; 52904 MW; AE207BEC68AD20D CRC64;

Query Match 56.2%; Score 1799; DB 2; Length 491;
Best Local Similarity 66.5%; Pred. No. 7,5e-111;
Matches 321; Conservative 44; Mismatches 112; Indels 6; Gaps 4;

QY 1 MLGVTVLGNALAGCGPPAPAPGQSGQCVHDCPALYPGPATLANAQCICGLRHIM 60
DB 1 MLGFFICVLA PASIGLSALAKLQPTGSGQCVHECFALFOGPATLDSQACQRLQHIM 60
QY 1 TVRSSVADVITSLILNDG-GVGRRLMTIGLPPGCCDPRKLGRLGFPQWVTGNNTSY 119
DB 1 TVRSSVADVITSLILNDG--WIGQLPQSCDDPVHLGLRGPQWVTGNNTSY 117
QY 120 SRMARLDINGAPLCPGLCVAVSAABATVPSEPIWEEOCEVADGFLCEFPAPATCRPLA 179
DB 120 SRMARPNQGTAPLCPGLCVTVSTATAEAPRGPAMBEKCEFTGTGFLCEFTASCRPLT 177
QY 118 SRMARPNQGTAPLCPGLCVTVSTATAEAPRGPAMBEKCEFTGTGFLCEFTASCRPLT 177
DB 118 SRMARPNQGTAPLCPGLCVTVSTATAEAPRGPAMBEKCEFTGTGFLCEFTASCRPLT 177
QY 180 VEP-GAAAANVTITGTPPAARGADFOALPVGSSAAVAPLGIQLMCTAPPAVOGHMARE 238
DB 178 VNTDPEPAHAISSITNTPFGVSGADFOALPVGSSAAVAPLGIQLMCTAPPAVOGHMARE 237
QY 239 ARGAMDCSVENGCGEHAACNAIPGARPCQCPAGALQADGRSCTAS-TQSCNDLCEHFCVPP 297
DB 238 ARGAMDCSVENGCGEHAACNAIPGARPCQCPAGALQADGRSCTAS-TQSCNDLCEHFCVPP 297
QY 238 ARGAMDCSVENGCGEHAACNAIPGARPCQCPAGALQADGRSCTAS-TQSCNDLCEHFCVPP 297
DB 238 ARGAMDCSVENGCGEHAACNAIPGARPCQCPAGALQADGRSCTAS-TQSCNDLCEHFCVPP 297
QY 298 NPDPGSGYSCMCEGYRLAADQHCEDVDGCLIEPSPQRCQVNTQGFEGECVAPNDLV 357
DB 298 NAEVPGSYSCMCEGYRLAADQHCEDVDGCLIEPSPQRCQVNTQGFEGECVAPNDLV 357
QY 358 DGECEVPEVDFRANCEYQCCPLNQTSTYLCVAGSAPAPIPHBPHRCQMFNCQTACPADCD 417
DB 358 DGECEVPEVDFRANCEYQCCPLNQTSTYLCVAGSAPAPIPHBPHRCQMFNCQTACPADCD 417
QY 418 PNTQASCECPGEGYLLDDGFICTDIDECENGFCGVCVCHNLPGTPECTICGPPSALARRHIGT 477
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QY 418 PNTQASCECPGEGYLLDDGFICTDIDECENGFCGVCVCHNLPGTPECTICGPPSALARRHIGT 477
DB 418 PNTQASCECPGEGYLLDDGFICTDIDECENGFCGVCVCHNLPGTPECTICGPPSALARRHIGT 477

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QY 478 DCD 480
DB 478 DCD 480

RESULT 10
P97883.RAT
ID P97883.RAT PRELIMINARY; PRT; 461 AA.
AC P97883;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thrombomodulin (Fragment).
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OC NCBI_TaxId=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Brain capillary;
RA Wang L., Tran N.D., Schreiber S.S., Zlokovic B.V.;
RL Submitted (Feb-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U90121; AB049723.1; -; mRNA.
DR HSSP; P07204; 1FGD.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR00152; Asx hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001491; Thrombomodulin.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF07645; EGF_Ca; 1.
DR PRINTS; PR00907; THROMBOMODULIN.
DR SMART; SM00179; EGF_Ca; 2.
DR PROSITE; PS00010; ASX_HYDROXYL_2.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS50026; EGF_3; 4.
DR PROSITE; PS01187; EGF_Ca; 2.
DR KW EGF-like domain.
DR NON TER 1
SQ SEQUENCE 461 AA; 49499 MW; 45971BCB84688E67 CRC64;

Query Match 50.0%; Score 1600; DB 2; Length 461;
Best Local Similarity 64.3%; Pred. No. 1e-97;
Matches 288; Conservative 44; Mismatches 110; Indels 6; Gaps 5;

QY 131 PLGCPICVAVSAABATVPSEPIWEEOCEVADGFLCEFPAPATCRPLAVERP-GAAAAA 188
DB 12 PLGCPICVTVSTATAEAPRGPAMBEKCEFTGTGFLCEFTASCRPLTNTDPEGAH 71
QY 189 VSITGTPFAARGADFOALPVGSSAAVAPLGIQLMCTAPPAVOGHMAREAPGAMDCSVE 248
DB 72 ISSITNTPDGVSAGADFOALPVGSSAAVAPLGIQLMCTAPPAVOGHMAREAPGAMDCSVE 131
QY 249 NGGCEHAACNAIPGARPCQCPAGALQADGRSCTAS-TQSCNDLCEHFCVPPDPGYSYC 307
DB 132 NGGCEHAACNAIPGARPCQCPAGALQADGRSCTAS-TQSCNDLCEHFCVPPDPGYSYC 191
QY 308 MCEGYRLAADQHCEDVDGCLIEPSPQRCQVNTQGFEGECVAPNDLVNDEGCEVPEVDP 367
DB 192 MCEGYRLAADQHCEDVDGCLIEPSPQRCQVNTQGFEGECVAPNDLVNDEGCEVPEVDP 251
QY 368 CFRANCEYQCCPLNQTSTYLCVAGSAPAPIPHBPHRCQMFNCQTACPADCPNTQASCECP 427
DB 252 CFRANCEYQCCPLNQTSTYLCVAGSAPAPIPHBPHRCQMFNCQTACPADCPNTQASCECP 311
QY 428 EGYLLDDGFICTDIDECENGFCGVCVCHNLPGTPECTICGPPSALARRHIGTDCDSGKY--D 485
DB 428 EGYLLDDGFICTDIDECENGFCGVCVCHNLPGTPECTICGPPSALARRHIGTDCDSGKY--D 485

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Db      312 EGFILDEGSICTDIDECSCQECLTNRCRNPGSYECICGPDOTALAGQISKDCDIPVLED 371
Qy      486 GCGSGSGEPPPS-PTPGSTLTPPAVLVHSGLLIGISIAS/CLVVALTALLCHRRKQGA 544
Db      372 SEGGSGSEHSSNTVVSSTVPSPAPMHSGLIGISIASLVALLALCHLRKQGT 431
Qy      545 ARAKMEYKCAPSKKVVLLQHVRTERTPO 572
Db      432 ARALEKTKTSSAKVALLQHVRTERTLQ 459

RESULT 11
TRBM BOVIN
ID TRBM BOVIN STANDARD; PRT; 356 AA.
AC P06579;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thrombomodulin (TM) (Fetomodulin) (Fragment).
GN Name=THBD;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87067408; PubMed=3024152;
RA Jackson R.W., Beeler D.L., Vandewater L., Rosenberg R.D.;
RT "Characterization of a thrombomodulin cDNA reveals structural
RT similarity to the low density lipoprotein receptor.";
RT Proc. Natl. Acad. Sci. U.S.A. 83:8834-8838(1986).
CC -1- FUNCTION: Thrombomodulin is a specific endothelial cell receptor
CC that forms a 1:1 stoichiometric complex with thrombin. This
CC complex is responsible for the conversion of protein C to the
CC activated protein C (protein Ca). Once evolved, protein Ca
CC activates the activated cofactors of the coagulation mechanism,
CC factor Va and factor VIII, and thereby reduces the amount of
CC thrombin generated.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Endothelial cells are unique in synthesizing
CC thrombomodulin.
CC -1- SIMILARITY: Contains 6 EGF-like domains.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL, M14657; AAA30785.1; -; mRNA.
CC PIR, A25918; A25918.
CC HSSP, P07204; 11MR.
CC SMR, P06579; 137-253.
CC InterPro, IPR000152; Asx hydroxyl_S.
CC InterPro, IPR000742; EGF_2.
CC InterPro, IPR001881; EGF_Ca bd.
CC InterPro, IPR006209; EGF-like.
CC InterPro, IPR001491; Thrombomodulin.
CC Pfam, PF00008; EGF_2.
CC Pfam, PF07645; EGF_CA; 1.
CC PRINTS, PR00907; THROMBOMODULIN.
CC SMART, SM00179; EGF_CA; 1.
CC PROSITE, PS00010; ASX_HYDROXYL_2.
CC PROSITE, PS00022; EGF_1; FALSE_NEG.
CC PROSITE, PS01186; EGF_2; 3.
CC PROSITE, PS50026; EGF_3; 3.
CC PROSITE, PS01187; EGF_CA; 2.
CC Blood coagulation; EGF-like domain; Glycoprotein; Receptor; Repeat;
CC Transmembrane.
KW TOPO_DOM 1 296 Extracellular (Potential).
FT TRANSMEM 297 320 Potential.
FT TOPO_DOM 321 356 Cytoplasmic (Potential).
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FT DOMAIN 17 57 EGF-like 1.
FT DOMAIN 60 98 EGF-like 2.
FT DOMAIN 99 137 EGF-like 3; calcium-binding (potential).
FT DOMAIN 139 179 EGF-like 4.
FT DOMAIN 178 214 EGF-like 5.
FT DOMAIN 215 254 EGF-like 6; calcium-binding (potential).
FT CARBOHYD 271 271 O-linked (Xyl. . .) (glycosaminoglycan) (By
FT similarity).
FT DISULFID 21 32 By similarity.
FT DISULFID 28 41 By similarity.
FT DISULFID 43 56 By similarity.
FT DISULFID 64 72 By similarity.
FT DISULFID 68 82 By similarity.
FT DISULFID 84 97 By similarity.
FT DISULFID 103 114 By similarity.
FT DISULFID 110 123 By similarity.
FT DISULFID 125 136 By similarity.
FT DISULFID 143 152 By similarity.
FT DISULFID 148 162 By similarity.
FT DISULFID 164 178 By similarity.
FT DISULFID 182 191 By similarity.
FT DISULFID 187 199 By similarity.
FT DISULFID 201 213 By similarity.
FT DISULFID 219 228 By similarity.
FT DISULFID 224 237 By similarity.
FT DISULFID 239 253 By similarity.
FT NON_TER 1 1
SQ SEQUENCE 356 AA; 37795 MW; 29B41F097ABE1093 CRC64;

Query Match 41.0%; Score 1314; DB 1; Length 356;
Best Local Similarity 65.0%; Pred. No. 6.4e-79;
Matches 232; Conservative 42; Mismatches 67; Indels 16; Gaps 7;

Qy 229 GAVGSHAREAPAGMDCSVENGCEHACNAIPGAPPCCPAGALLODGRSC-TASTQSC 287
Db 5 GETGRSRKREAPGAMACVERGCGHCKSGAGSNCLCPADALQADGRSCGPAEHIPC 64
Qy 288 NDLCSEHFCVNPDPGYSCKCTGYRIADQHRCEVDCTLEPSPQRCVNTQSGFE 347
Db 65 HQLCSEHFC--HILHIGLVNTTCICEAGYOLADQHRCEVDCAOLPSPQRCVNTQSGFQ 122
Qy 348 CHCTPNTDLDNGCEVPPDPREFRANCEGCOPLNQTSLYCVAGSAPFAPHPHRCQWFC 407
Db 123 CHCTPVELVDGECVDPVPCFNNCEYQCPVRSSEKCTCAGFAVPAAPPHKQWFC 182
Qy 408 NOTACPADCPNTQASCEPGEYILDGFTCTDIDECENGSGFCGVCNLTPTPECICGP 467
Db 183 NOTSCPADCPHYPTICRCPGGYIIDSGTCTDINECDT-NICPGQCNTLPQTEYCICGP 241
Qy 468 DSALARRHIGTDCDSGKV-----DGGDSCSGEPPSPPTGSLTP-PA-VGLVHSGLL 517
Db 242 DSALSGQIGIDCDPDVQVNEERGTPEDYG--SGGEPPVSPTRGAVTARPSPAAGPLHSGVL 299
Qy 518 IGISIAS/CLVVALTALLCHLRKQGAARAKMEYKCAPSKKVVLLQHVRTERTPORTL 574
Db 300 VGISIASLVALLALCHLRKQGSRGLETKCVPAKELMLQGVKXTERTPQKL 356

RESULT 12
Q4SWS2_TETNG PRELIMINARY; PRT; 496 AA.
ID Q4SWS2_TETNG
AC Q4SWS2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAPI3541, whole genome shotgun sequence.
GN ORFNAMES=GSTENG00011332001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Necteleostei; Necteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphae; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
```

[1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ouzf-Costaz C., Bernot A.,
 RA Nicud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castell V., Katinka N., Vacherie B.,
 RA Biemont C., Skalli Z., Catolico L., Poulain J., De Bernardis V.,
 RA Parra G., Lardier G., Brottier P., Coutanceau J.P., Guzy J.,
 RA Kellis M., Volff J.N., Guigo R., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lauder V., Schachter V., Queller F., Sautin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAB0103541; CAF94910.1; -; Genomic DNA.
 CC SEQUENCE 496 AA; 52663 MW; 1B270211A7A5C95A CRC64;
 SQ
 Query Match 20.3%; Score 651.5; DB 2; Length 496;
 Best Local Similarity 35.1%; Pred. No. 5.7e-35;
 Matches 146; Conservative 40; Mismatches 143; Indels 87; Gaps 15;
 QY 24 QGGGSCVCEHDCPALYPGATFLNASSQICDGLRGHLMTVSSVADVISLLNGGCGYGR 83
 DB 23 KPSSGYCIGNOCFTASBQETFAAQKECGJGGLMTVTSVSHDIVSLLGVSQ--- 79
 QY 84 RRLWIGLQLPPCGCDPKRLGFLRGFWMTGDNNTSYSRMARLDLNGAPLGCPLCAVSAEA 143
 DB 80 -RFPIGHLPLTACDGSU--ELNGFSWVPGSSESPFMSWPAAPDGC--SSDRCVSVSPV 134
 QY 144 EATVPSEPIWEQCEVADGFLCEFHFPATCRPLAVEPAAAAAVSITTYGTPFAARGAD 203
 DB 135 D-----PFKMTREPCDAAAGFLCEFGFNTCRGL-----GAGAGTPTTSTPIGIEGGE 184
 QY 204 FQALPVSSAAVAVLGLQIMCTAPPGAVQGHMAREAPCAMDCSVENGCCEHACNAIPAR 263
 DB 185 LLSLPSPGSAVALMPSGSKYIC-----FSGGAV--EAP--WTCEVLGGGCEHRCCTLDPEOM 235
 QY 264 P-CGCPAGAAAL-----OAGRSCTASTOSCNULDCEHFCVNPDPDQSGSCMCETGY 313
 DB 236 PLCTCPKQGTNPENQVTCBAQDPCHALR-----CAHACY--DNGSSHACKRGGF 286
 QY 314 RLAAOHRCEBDVDDCILEPSPQRCVNTQGGFEGCHYPNYDLVDGECVBEVDPCFRANC 373
 DB 287 KLAADGRSCVVDVDCV--SAPCEHCKNSPGSYKACACSGY-RVDAK----- 330
 QY 374 EYQCOPLNQTSTYLCVCAEGFAPIPHEPRRCMFCNQTACPADCDPNTQASCECEBG 429
 DB 331 -----BPHRCQLHCECECAECAPQGVHLLRGG 361
 RESULT 13
 QATSR2_TESTING PRELIMINARY; PRT; 431 AA.
 AC QATSR2;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DS Chromosome undetermined SCAF9151, whole genome shotgun sequence.
 DN (Fragment).
 GN ORFNames=STENG0006679001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ouzf-Costaz C., Bernot A.,
 RA Nicud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castell V., Katinka N., Vacherie B.,
 RA Biemont C., Skalli Z., Catolico L., Poulain J., De Bernardis V.,
 RA Parra G., Lardier G., Brottier P., Coutanceau J.P., Guzy J.,
 RA Kellis M., Volff J.N., Guigo R., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lauder V., Schachter V., Queller F., Sautin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAB01009151; CAF91770.1; -; Genomic DNA.
 CC NON TER 1 431
 FT NON TER 1 431
 FT SEQUENCE 431 AA; 47647 MW; 7CC0872B307085A8 CRC64;
 SQ
 Query Match 18.9%; Score 604.5; DB 2; Length 431;
 Best Local Similarity 33.2%; Pred. No. 6.4e-32;
 Matches 151; Conservative 49; Mismatches 182; Indels 73; Gaps 20;
 QY 30 CVEDHCPALYGPATFLNASSQICDGLRGHLMTVSSVADVISLLNGDGVGRRRL-- 86
 DB 17 CTDDGCFVWHFQRTFLFESWRSCKDNGNGLAIIRKEDAGTIGRLFASADLRHSTTKQA 76
 QY 87 WIGLQL-PPCGCDPKRLGFLRGFWMTGDNNTSYSRMARLDLNGAPLGCPLCAVSAEA 145
 DB 77 WIGLQHRHROCSALU--PLRGFSWTTGDDDTDTTMMGEGSPACL-APFCVAVV-YDA 131
 QY 146 TVPSEPI-WEQCEVADGFLCEFHFPATCRPLAVEPAAAAAVSITTYGTPFAARGAD 204
 DB 132 QKRSNLIKMTVDGFCVAHTDGLCHYAVGCMPTLRSE-GAGKA-----LYTPFLHRLTL 186
 QY 205 QALVGSAAV-APLGLQ---LMCTAPPGAVQGHMAREAPG-----WDGSENGG 251
 DB 187 TLVPPGTVAATLPSPDTERESSVLTCTLRDGL-ARMSRNDQFPGSGPVSRRH-CVDNNG 244
 QY 252 CEHACNAIPARPCGCPAGAAALQADGRSCTASTOSCNULDCEHFCVNPDPDQSGSCMCET 311
 DB 245 CEHFCRAAGVNFCECAGYQLAAGNQCEPLDVCKSPCKFEELPISD---SYRCACPD 301
 QY 312 GYRLAADHRCEBDVDDCILEPSPQRCVNTQGGFEGCHYPNYDL-VDGECVBEVDPCFR 370
 DB 302 GYMLAPBEHCDMDVDEL--QSPCEHLCVNSPSPGFCRCHRYLLDEGAC-ELADGEMA 358
 QY 371 ANCEYOCOPLNQSTYLCVCAEGFAPIPHEPRRCMFCNQTACPADCDPNTQASCECEBG 430
 DB 359 NPCEHACEN-TAGSHVCHGELGFSPIPEDPSRCQ----- 391
 QY 431 ILDDGFLCTDIDCEGNGPFGSGVCHNLPGTFECTC 465
 DB 392 -----DTDECRMAGTQOQICVNFGSGFQCYC 417
 RESULT 14
 OS9EB6_HUMAN
 ID OS9EB6_HUMAN PRELIMINARY; PRT; 671 AA.
 AC OS9EB6;

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DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Complement component 1, q subcomponent, receptor 1 variant
   (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta endothelial cell;
RA Tsuchi Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB209895; BAD93132.1; -; mRNA.
DR Ensembl; ENSG00000125810; Homo sapiens.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca bd.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF07645; EGF_CA; 3.
DR Pfam; PF00059; lectin_C.1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 5.
DR SMART; SM00179; EGF_CA; 5.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS50026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 3.
DR Receptor.
KW NON TER.
FT
SQ SEQUENCE 671 AA; 70460 MW; 00CCDBC6CEBA063 CRC64;

Query Match 18.6%; Score 597; DB 2; Length 671;
Best Local Similarity 30.9%; Pred. No. 3.1e-31;
Matches 181; Conservative 54; Mismatches 205; Indels 146; Gaps 31;

12 LAGGFPPARF-----PQSGSQ-----CQEHDCFALYRGP 42
13 LSPGFSPPAEGHTETGMATSMGILLILLITLTPGAGTADTEAVVCVGTACTYAHSGK 62
3 LSPGFSPPAEGHTETGMATSMGILLILLITLTPGAGTADTEAVVCVGTACTYAHSGK 62
43 ATPFNASQICDGLRHLMTVRSSVAAD---VISLLNGDGVGR--RLMTGLQLPFG- 95
63 LSAAEAOHCHONONGENLATVRSKEAYOVYLAQLRLREALTRMRKSPNIGLOREK 122
96 CGDPRRLPLRGFQVNTDNNITSYSRMARLDLNGAPLGCPLVA--VSAEAETVSE-PI 152
123 CLDPSL-PLKGFSSVVGSGEDTPYSGNMHKEKLNSC--ISKVCSLLDLSQPLSRLPK 178
153 WEBOQC-----EYKADGFLCEFHFPATCRPLAV-EPGAAAANVSITGTPRANAGAPQ 205
179 WSEGCSPGSPGSPGSIIEGVCKFSFKMGCRPLALGPG-----QVYTTTPQTSSSIE 232
206 ALPVSSAAVAPLIGQLMC-TAPGAVGGM---ARAPGAMD-----CSV 247
233 AVPPASAAVNA-----CGEGDKDETQSHYFLCKEKADVDVWGSSGFLCSPKYGCVF 285
248 ENGGESEHAC-NAIPGAPCCQCPAGALQADRSCTASTOSCNLDCE--HFCVNPDPQGS 304
286 NNGGCHQCFCBGDSSPLCGCRPRRLDDVLDTASRNPCSSPFGAGATVIGP-HGKN 344
305 YSCMCETGYRLAADHRCEDVDCLIEBSPQRCVCVNTGGEGCHCYPNYDLVDGCVBP 364

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Db 345 YTCRCPGCGYQLDSSQLDCVUDDEC--QDSPCAQECVNTPGFRCCEWVG-----EP 394
Qy 365 VDPCEFRANCEYOCPLNQTSTYLVCYACAGFAPIPHEPRQCFNCQTACPADCDNTQAS- 423
Db 395 GGF-----GGGACQDVDE-----CALGRSP-----CAQGC-TNTDGSF 426
Qy 424 -CECPGEGYIL--DDGFICTDIDEC--ENGFCSCVCHNLRTFECTICGPDALARRHIGTD 478
Db 427 HCSCEEGYVLAGEBDQTCQOVDECVGPGGLCSLCSNTGGSFRCGLPGWVLPN-GVS 485
Qy 479 CDGSKV-----DGGDSSSGE-----PPSPPTGSTRPPA 508
Db 486 CTWGPVSLGPPSGPPDEEDKSEKSGSTVPPRAATSPTRBEGTPKA 531

RESULT 15
ClORI_HUMAN
ID ClORI_HUMAN STANDARD, PRT; 652 AA.
AC Q9NPY3; Q00274;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Complement component C1q receptor precursor (complement component 1, q
DE subcomponent, receptor 1) (C1qR) (C1qR(p)) (C1q/MBL/SPA receptor)
DE (CD93 antigen) (CDW93).
DE Name=C1OR1; Synonyms=CD93;
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN
RX MEDLINE=97199258; PubMed=9047234; DOI=10.1016/S1074-7613(00)80419-7;
RX Neomunceno R.R., Henschel-Bdman A.H., Burgess W.H., Temner A.J.,
RX "cDNA cloning and primary structure analysis of C1qR(p) in human
RX C1q/MBL/SPA receptor that mediates enhanced phagocytosis in vitro.";
RX Immunity 6:119-129(1997).
[2]
RN
RP NUCLEOTIDE SEQUENCE, AND VARIANT ALA-318.
RX MEDLINE=21640567; PubMed=11781389;
RX Steinberger P., Szekeres A., Wille S., Stockl J., Selenko N.,
RX Prager E., Staffler G., Madic O., Stockinger H., Knapp W.;
RX "Identification of human CD93 as the phagocytic C1q receptor (C1qR)
RX by expression cloning.";
RX J. Leukoc. Biol. 71:133-140(2002).
[3]
RN
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RX Deloukas F., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RX Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggaley C.L.,
RX Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RX Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RX Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RX Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RX Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cordy N.R.,
RX Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RX Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RX Gething D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RX Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Johnson D.,
RX Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RX Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RX Lehaeaeiaho M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RX Marsh V.L., Martin S.L., McConachie L.J., McEay K., McMurtry A.A.,
RX Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RX Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RX Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
RX Rice C.M., Ross M.T., Scott C.E., Senta H.K., Showkenen R., Sims S.,
RX Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Suleston J.B.,
RX Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RX Tracey A., Tromans A.C., Trollin M., Wall M., Wallis J.M.,
RX Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RX Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

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